WEST Search History

DATE: Wednesday, October 08, 2003

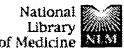
Set Name Query side by side			Hit Count Set Nam result set		
DB=USI	PT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ				
L20	L19 AND transforming	62	L20		
L19	L18 AND growth-factor	75	L19		
L18	TGFb OR TGF-b OR TGFbeta OR TGF-beta	6726	L18		
L17	transforming-growth-factor-beta	4	L17		
L16	L15 AND beta	208	L16		
L15	L12 AND TGF	220	L15		
L14	L12 AND transforming-growth-factor	0	L14		
L13	L12 AND tumor-growth-factor-beta	0	L13		
L12	((530/300)!.CCLS.)	2862	L12		
L11	L9 AND L10	34	L11		
L10	fusion-protein OR chimeric-protein	254	L10		
L9	L8 AND mature	1711	L9		
L8	L5 AND L7	2084	L8		
L7	TGFb OR TGF-b OR TGFbeta OR TGF-beta	6726	L7		
L6	L5 AND TGF-b	86	L6		
L5	L4 AND TGF	2617	L5		
L4	((435/69.1 435/69.7 435/252.3 435/254.2 435/325)!.CCLS.	24768	L4		
L3	Wolfraim.IN.	0	L3		
L2	Letterio.IN.	19	L2		
L1	(Wolfraim.IN.)	0	L1		

END OF SEARCH HISTORY

Entrez-PubMed Page 1 of 10





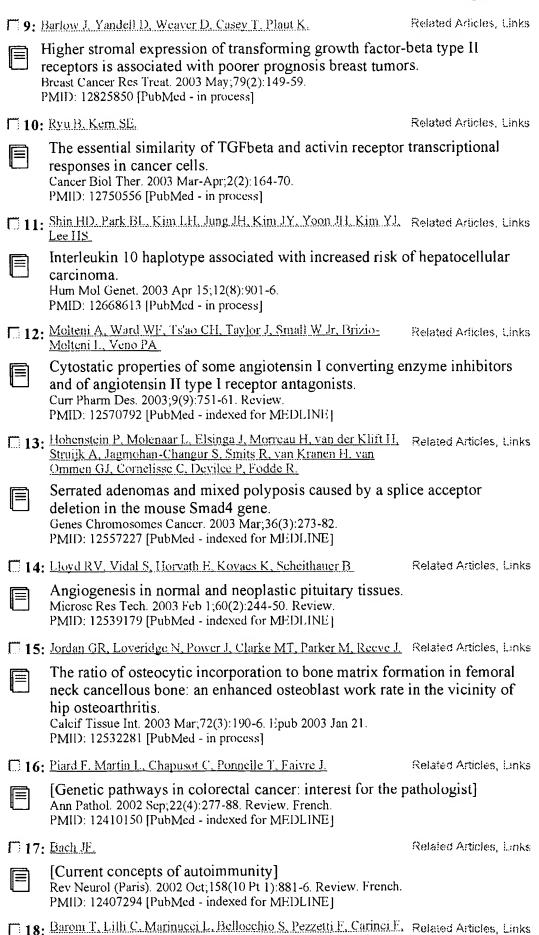


			max non handle		())	medicine 🛋	246.00		
PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Boo	
Search PubMed	i 🖳	for TGFb				Go Clear			
A.S		Limits	Preview/Index	Histo	ory	Clipboard	De	tails	
About Entrez)	splay Summa	n/ :==	oz [200]	I I Sort		to Text		
·			s 1-83 of 83	Show: 200	Solt			e page	
Text Version			m A, Song K, Oga	wa T. Wu R. N	Nichimura I		One	Links	
Entrez PubMed Overview Help FAQ Tutorial	_	Oral fibrob accelerates J Biol Chem.	last expression the collagen ge 2003 Oct 3 [Epub	of wound in al contraction ahead of print	nducible to n in vitro.	ranscript-3.0 ((wit3.0)		
New/Noteworthy E-Utilities		PMID: 1452	7947 [PubMed - as	supplied by p	oublisher]				
matakan di Samalana		2: Eng C.				Ref	ated Articles	, Links	
PubMed Services Journals Database MeSH Database Single Citation Mate	cher	Am J Med G	on, polyps, or ca enet. 2003 Nov 1; 8069 [PubMed - in	122A(4):315-2		ct your future	.		
Batch Citation Matc Clinical Queries		3: Juhan-Vague	I, Morange PE, A	lessi MC.		Rel	ated Articles	, Links	
LinkOut Cubby Related Resourc	~	The insulin resistance syndrome: implications for thrombosis and cardiovascular disease.							
Order Documents	,		9655 [PubMed - in		, , ,				
NLM Gateway TOXNET Consumer Health		4: Marchand-A Y, Leseche C	dam S. Marchal J. 3. Valeyre D. Mal	Cohen M. Sol H. Aubier M.	er P. Gerard Dehoux M.	LB <u>, Castior</u> Rel <u>Crestani B</u>	ated Articles	, Links	
Clinical Alerts ClinicalTrials.gov PubMed Central Privacy Policy		pulmonary Am J Respir	nepatocyte grow fibrosis. Crit Care Med. 20 7024 [PubMed - as	03 Aug 28 [Ep	oub ahead of		idiopathi	С	
	Г	5: Davies JA.				Rel	ated Articles	i, Links	
		ScientificWo	nesis of the met orldJournal. 2002 J 0322 [PubMed - in	un 28;2(6):193					
	Γ	6: Xu L, Alarco	on C. Col S. Massa	gue J.		Rel	ated Articles	, Links	
		and nuclea J Biol Chem.	omain utilization r import. 2003 Aug 13 [Epi 7407 [PubMed - as	ub ahead of pr	int]	l4 for nucleop	orin intera	action	
	Γ.	7: <u>Li G. Wang</u>	S, Gelehrter TD.			Rel	ated Articles	, Links	
		transrepre	ession						
	Γ.	8: Zhou H. Lan	iont SJ.			Rel	ated Articles	, Links	

Association of transforming growth factor beta genes with quantitative trait loci for antibody response kinetics in hens.

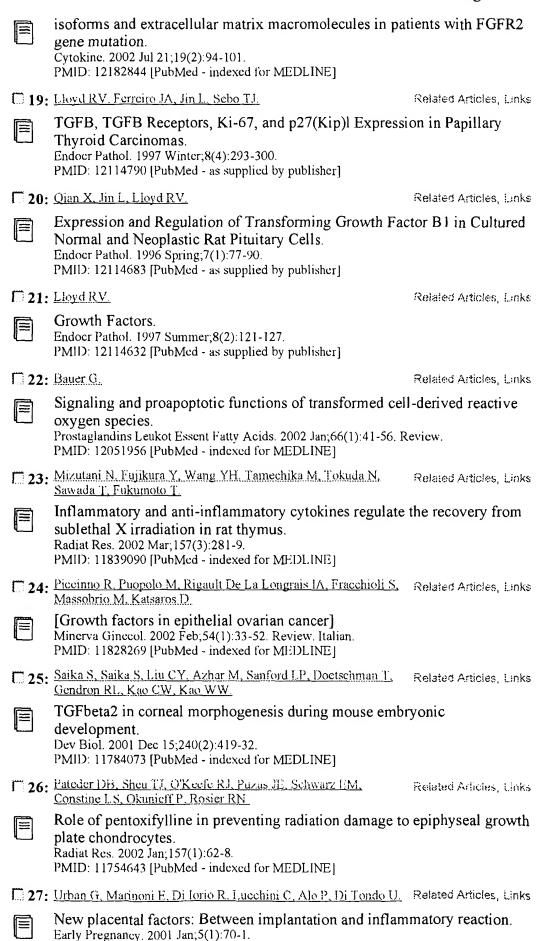
Anim Genet. 2003 Aug;34(4):275-82.

PMID: 12873215 [PubMed - in process]



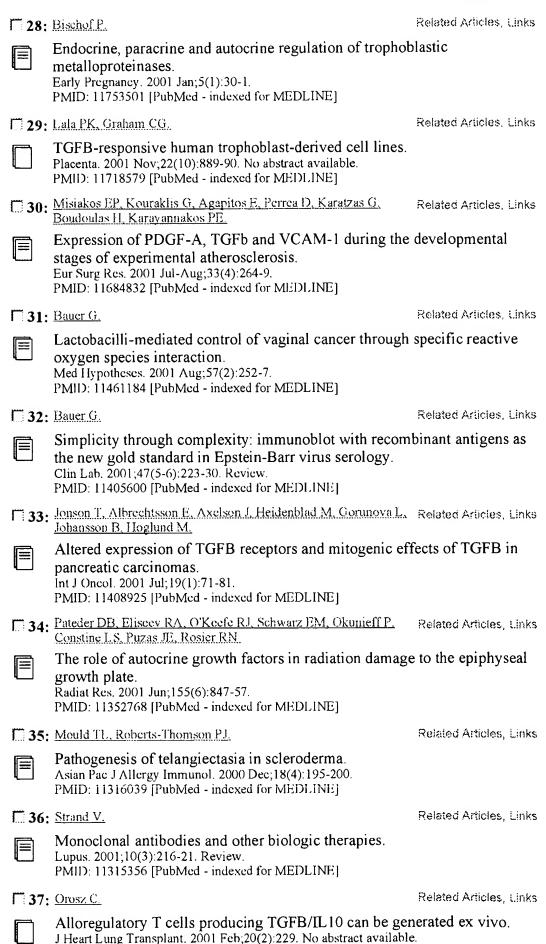
Crouzon's syndrome: differential in vitro secretion of bFGF, TGFbeta I

Stabellini G. Balducci C, Locci P.



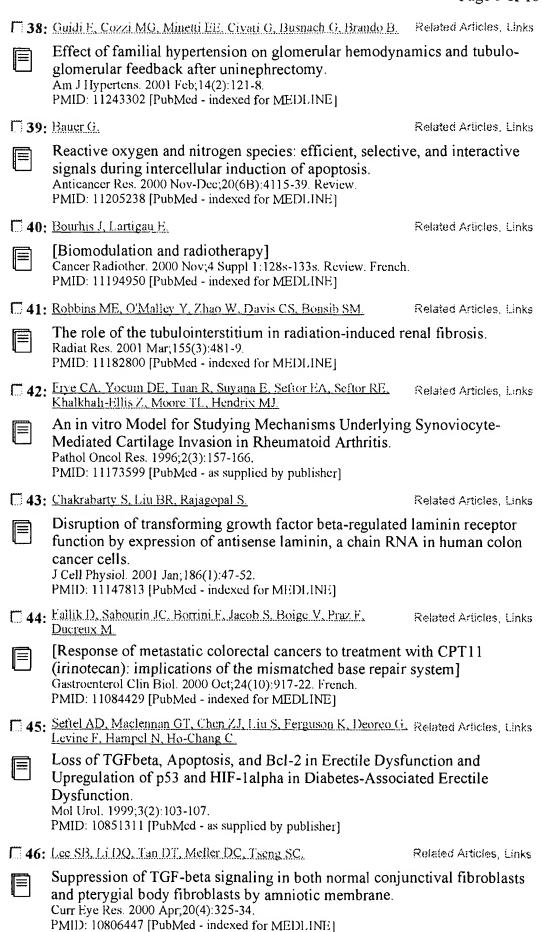
PMID: 11753520 [PubMed - indexed for MEDLINE]

Entrez-PubMed Page 4 of 10



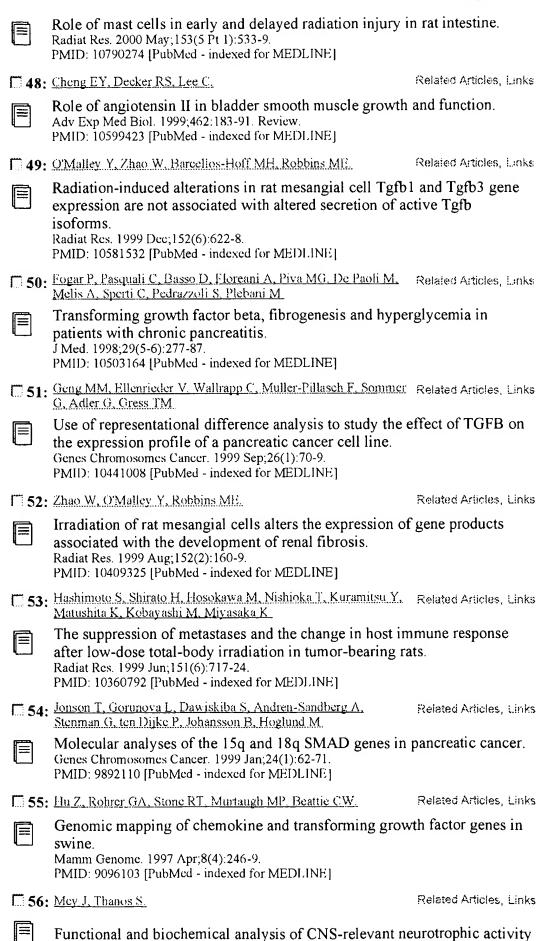
PMID: 11250438 [PubMed - as supplied by publisher]

Entrez-PubMed Page 5 of 10



47: Zheng H, Wang J, Hauer-Jensen M.

Entrez-PubMed Page 6 of 10



in the lesioned sciatic nerve of adult rats.

J Hirnforsch. 1996;37(1):25-50.

Entrez-PubMed Page 7 of 10

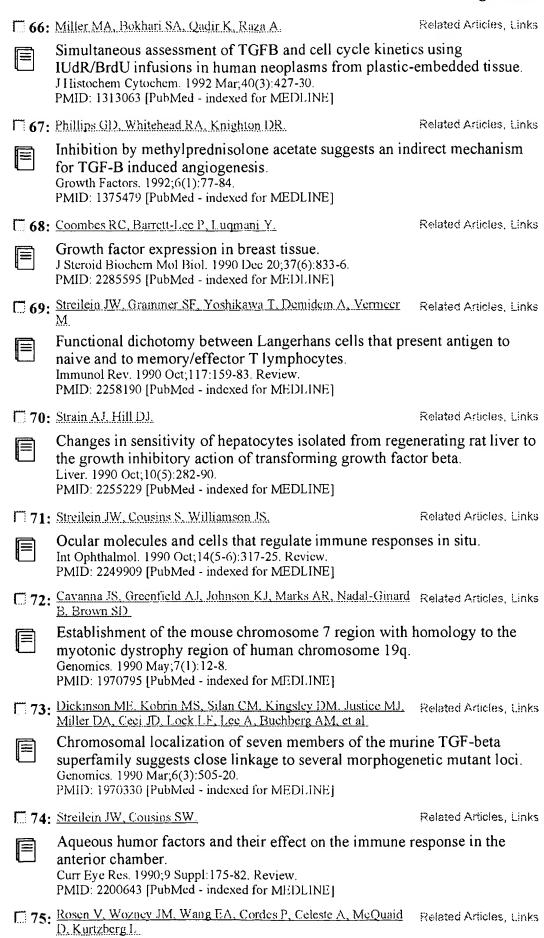
PMID: 8964975 [PubMed - indexed for MEDLINE] 57: Ace Cl. Okulicz WC. Related Articles, Links Differential gene regulation by estrogen and progesterone in the primate endometrium. Mol Cell Endocrinol. 1995 Nov 30;115(1):95-103. PMID: 8674869 [PubMed - indexed for MEDLINE] 58: Spanakis E. Brouty-Boye D. Related Articles, Links Quantitative variation of proto-oncogene and cytokine gene expression in isolated breast fibroblasts. Int J Cancer. 1995 May 29;61(5):698-705. Erratum in: Int J Cancer 1995 Nov 15;63 PMID: 7768644 [PubMed - indexed for MEDLINE] 59. Bhattacharyya N, Ramsammy R, Eatman E, Hollis VW, Anderson Related Articles, Links <u>WA.</u> Protooncogene, growth factor, growth factor receptor, and estrogen and progesterone receptor gene expression in the immature rat uterus after treatment with estrogen and tamoxifen. J Submicrosc Cytol Pathol. 1994 Apr;26(2):147-62. PMID: 8019941 [PubMed - indexed for MEDLINE] [60: Williams ΔC, Hague A, Manning ΔM, Van der Stappen JW, Related Articles, Links Paraskeva C In vitro models of human colorectal cancer. Cancer Surv. 1993;16:15-29. Review. PMID: 8348534 [PubMed - indexed for MEDLINE] Related Articles, Links 61: Mathews I.S. Vale WW. Molecular and functional characterization of activin receptors. Receptor. 1993 Fall;3(3):173-81. Review. PMID: 8167568 [PubMed - indexed for MEDLINE] Related Articles, Links 62: Allannie H. Guilhem I. Maugendre D. [Is thyroid hormone useful in the prevention of nodular recurrence after hemithyroidectomy?] Ann Endocrinol (Paris). 1993;54(4):286-90. Review. French. PMID: 8092805 [PubMed - indexed for MEDLINE] 63: Stampfer MR, Yaswen P. Related Articles, Links Culture systems for study of human mammary epithelial cell proliferation, differentiation and transformation. Cancer Surv. 1993;18:7-34. Review. PMID: 8013001 [PubMed - indexed for MEDLINE] [64: Hendricks-Taylor LR, Bachinski LL, Siciliano MJ, Fertitta Δ, Related Articles, Links Trask B, de Jong P.J. Ledbetter DH, Darlington GJ The CCAAT/enhancer binding protein (C/EBP alpha) gene (CEBPA) maps to human chromosome 19q13.1 and the related nuclear factor NF-IL6 (C/EBP beta) gene (CEBPB) maps to human chromosome 20q13.1. Genomics. 1992 Sep;14(1):12-7. PMID: 1427819 [PubMed - indexed for MEDLINE] 65: Lee SW, Tomasetto C, Paul D, Keyomarsi K, Sager R. Related Articles, Links

J Cell Biol. 1992 Sep;118(5):1213-21. PMID: 1324944 [PubMed - indexed for MEDLINE]

communication in human mammary tumor cell lines.

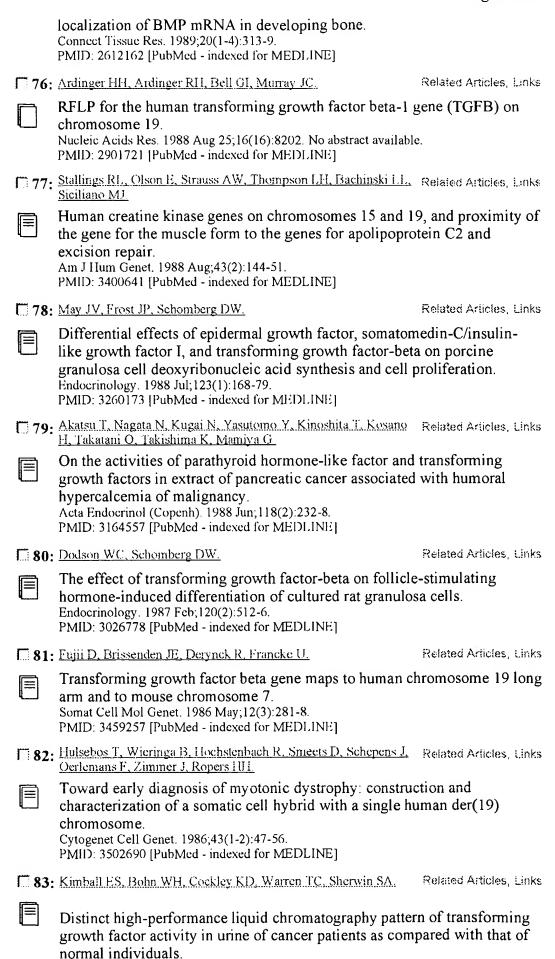
Transcriptional downregulation of gap-junction proteins blocks junctional

Entrez-PubMed Page 8 of 10



Purification and molecular cloning of a novel group of BMPs and

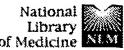
Entrez-PubMed Page 9 of 10



Cancer Res. 1984 Aug;44(8):3613-9.







of Medicine NEW Protein Structure PMO MIMO Taxonomy Book Search PubMed • for Itransforming growth factor beta AND tag Go Clear Preview/Index History Clipboard Details About Entrez Display Summary Show: 200 Sort Send to Text Items 1-26 of 26 One page. Text Version 1. Cao W, Mattagajasingh SN, Xu H, Kim K, Fierlbeck W, Deng J. Related Articles, Links Lowenstein CJ, Ballermann BJ Entrez PubMed Overview TIMAP, a novel CAAX box protein regulated by TGF-beta1 and expressed Help | FAQ in endothelial cells. Tutorial Am J Physiol Cell Physiol. 2002 Jul;283(1):C327-37. New/Noteworthy PMID: 12055102 [PubMed - indexed for MEDLINE] E-Utilities 2: Lin W, Zhang N, Qin R. Related Articles, Links PubMed Services Journals Database [Effect of aldose reductase expression by transforming growth factor-beta1 MeSH Database on rat mesangial cell] Single Citation Matcher Zhonghua Yi Xue Za Zhi. 2001 Jun 25;81(12):744-7. Chinese. Batch Citation Matcher PMID: 11798960 [PubMed - indexed for MEDLINE] Clinical Quenes LinkOut 1 3: Melhuish TA, Gallo CM, Wotton D. Cubby Related Articles, Links TGIF2 interacts with histone deacetylase 1 and represses transcription. Related Resources J Biol Chem. 2001 Aug 24;276(34):32109-14. Epub 2001 Jun 26. Order Documents PMID: 11427533 [PubMed - indexed for MEDLINE] NLM Gateway TOXNET 4: Breitkopf K, Lahme B, Tag CG, Gressner AM. Related Articles, Links Consumer Health Clinical Alerts Expression and matrix deposition of latent transforming growth factor beta ClinicalTrials gov binding proteins in normal and fibrotic rat liver and transdifferentiating PubMed Central hepatic stellate cells in culture. Hepatology. 2001 Feb;33(2):387-96. Privacy Policy PMID: 11172340 [PubMed - indexed for MEDLINE] 5: Gomez-Escobar N, Gregory WF, Maizels RM. Related Articles, Links Identification of tgh-2, a filarial nematode homolog of Caenorhabditis elegans daf-7 and human transforming growth factor beta, expressed in microfilarial and adult stages of Brugia malayi. Infect Immun. 2000 Nov;68(11):6402-10. PMID: 11035752 [PubMed - indexed for MEDLINE] 6: Ji X, Chen D, Xu C, Harris SE, Mundy GR. Yoneda T. Related Articles, Links Patterns of gene expression associated with BMP-2-induced osteoblast and adipocyte differentiation of mesenchymal progenitor cell 3T3-F442A. J Bone Miner Metab. 2000;18(3):132-9. PMID: 10783846 [PubMed - indexed for MEDLINE] 7: Bassuk JA, Pichler R, Rothmier JD, Pippen J, Gordon K, Meek RL, Related Articles, Links Bradshaw AD, Lombardi D, Strandjord TP, Reed M, Sage EH, Couser WG, Johnson R

8: Maroulakou IG, Shibata MA, Anyer M. Jorcyk CL, Liu M, Roche Related Articles, Links N. Roberts AB, Tsarfaty I, Reseau J, Ward J, Green JE

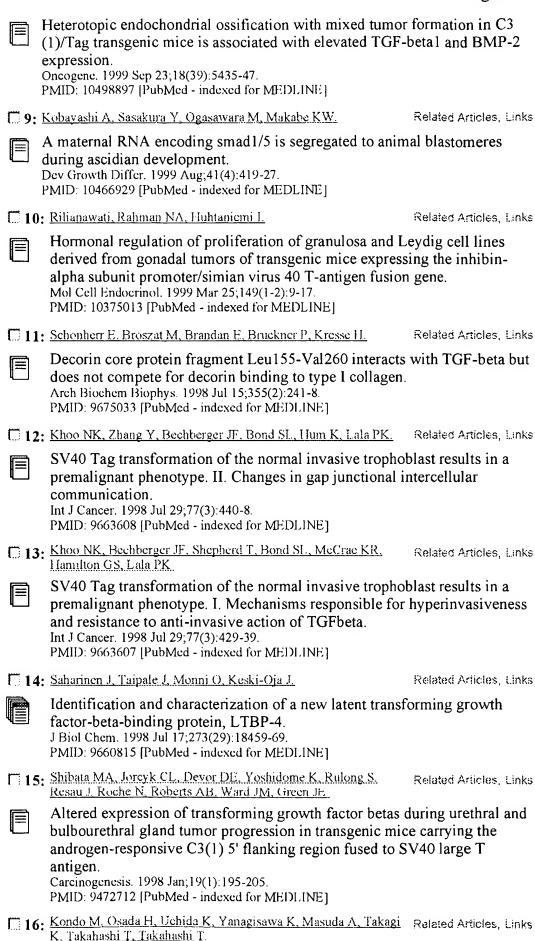
of glomerulonephritis.

Kidney Int. 2000 Jan;57(1):117-28.

PMID: 10620193 [PubMed - indexed for MEDLINE]

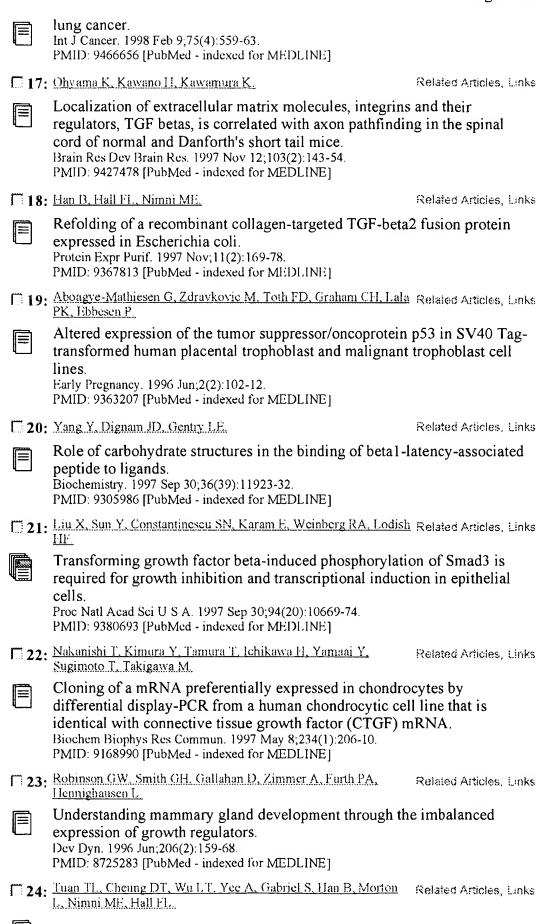
Induction of TGF-betal by the matricellular protein SPARC in a rat model

Entrez-PubMed Page 2 of 4



Molecular cloning of human TAK1 and its mutational analysis in human

Entrez-PubMed Page 3 of 4



Engineering, expression and renaturation of targeted TGF-beta fusion

⊫∣

proteins.

Connect Tissue Res. 1996;34(1):1-9

Entrez-PubMed Page 4 of 4

Items 1-26 of 26

PMID: 8835843 [PubMed - indexed for MEDLINE]

25: Henis YI, Moustakas A, Lin HY, Lodish HF.

The types II and III transforming growth factor-beta receptors form homoligomers.

J Cell Biol. 1994 Jul;126(1):139-54.

PMID: 8027173 [PubMed - indexed for MEDLINE]

26: Moses III..

Related Articles, Links

TGF-beta regulation of epithelial cell proliferation.

Mol Reprod Dev. 1992 Jun;32(2):179-84. Review.

PMID: 1637556 [PubMed - indexed for MEDLINE]

Display Summary

Show: 200 Sort Send to Text

Write to the Help Desk
NCB! | NLM | NIH
Department of Health & Human Services
Freedom of Information Act | Disclaimer

(0.12.2003/18:06:20

One page.

```
Connecting via Winsock to STN
Welcome to STN International!
                                   Enter x:x
 * * * * * * * * * Welcome to STN International
                                                           तेर तेर तेर तेर तेर तेर तेर तेर तेर
* * * * * * * * * * * * * * STN Columbus
                                              FILE 'HOME' ENTERED AT 15:15:48 ON 08 OCT 2003
=> file CAPLUS
=> s transforming-growth-factor-beta OR TGFb
          49811 TRANSFORMING
        1080382 GROWTH
           4000 GROWTHS
        1082449 GROWTH
                   (GROWTH OR GROWTHS)
         796671 FACTOR
         699815 FACTORS
        1260069 FACTOR
                   (FACTOR OR FACTORS)
        1218606 BETA
           1326 BETAS
        1218672 BETA
                   (BETA OR BETAS)
          20853 TRANSFORMING-GROWTH-FACTOR-BETA
                   (TRANSFORMING(W)GROWTH(W)FACTOR(W)BETA)
            148 TGFB
              2 TGFBS
            149 TGFB
                   (TGFB OR TGFBS)
L1
          20928 TRANSFORMING-GROWTH-FACTOR-BETA OR TGFB
=> S L1 AND fusion
         219978 FUSION
           8229 FUSIONS
         224412 FUSION
                   (FUSION OR FUSIONS)
L2
            419 L1 AND FUSION
=> S L2 AND functional
         403209 FUNCTIONAL
           3240 FUNCTIONALS
         404142 FUNCTIONAL
                   (FUNCTIONAL OR FUNCTIONALS)
L3
             40 L2 AND FUNCTIONAL
=> S L2 AND mature
          85437 MATURE
            935 MATURES
          86202 MATURE
                   (MATURE OR MATURES)
L4
             27 L2 AND MATURE
=> D L3 1-40
L3
     ANSWER 1 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     2003:656937
                    CAPLUS
AN
DN
     139:193621
     Reversible oxidation of protein tyrosine phosphatases and its detection by
TI
     study of signal transduction pathways
IN
     Tonks, Nicholas K.; Meng, Tzu-Ching; Cool, Deborah E.
     Cold Spring Harbor Laboratory, USA; Ceptyr, Inc.
PA
SO
     PCT Int. Appl., 238 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN.CNT 1
     PATENT NO.
                        KIND
                               DATE
                                                APPLICATION NO.
                                                                   DATE
                                                 ------
                               20030821
PΙ
     wo 2003068984
                         Α2
                                                WO 2003-EP1446
                                                                   20030213
              AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
              CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ,
              UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD,
```

RU, TJ, TM

```
CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2002-356810P
                          Р
                                  20020213
      US 2003-366547
                            Α
                                  20030212
L3
      ANSWER 2 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2003:360779 CAPLUS
AN
DN
      138:380400
      TAK1-TAB1
                    ***fusion***
                                      protein: a novel constitutively active
TI
      mitogen-activated protein kinase kinase kinase for use in drug screening
IN
      Sugita, Naohisa; Sakurai, Hiroaki; Sato, Naoya
PA
      Tanabe Seiyaku Co., Ltd., Japan
SO
      Jpn. Kokai Tokkyo Koho, 34 pp.
      CODEN: JKXXAF
DT
      Patent
      Japanese
LA
FAN.CNT 1
      PATENT NO.
                          KIND
                                 DATE
                                                    APPLICATION NO.
                                                                        DATE
PΙ
      JP 2003135070
                                  20030513
                            Α2
                                                    JP 2001-335988
                                                                        20011101
PRAI JP 2001-335988
                                  20011101
      ANSWER 3 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
      2003:334937 CAPLUS
AN
      138:349696
DN
         ***Fusion***
                          protein comprising cytokines, chemokines, and interferons
TI
      for use as vaccine adjuvant in immunotherapy for cancer and viral
      infection
      Galipeau, Jacques; Stagg, John
Centre for Translational Research In Cancer, Can.
IN
PA
SO
      PCT Int. Appl., 53 pp.
      CODEN: PIXXD2
DT
      Patent
      English
LA
FAN.CNT 1
      PATENT NO.
                          KIND DATE
                                                   APPLICATION NO. DATE
                                  20030501
PΙ
      wo 2003035105
                           Α2
                                                   WO 2002-CA1649
                                                                        20021023
               AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD,
                RU, TJ, TM
           RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
                CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
                PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
                NE, SN, TD, TG
PRAI US 2001-330476P
                                  20011023
L3
      ANSWER 4 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      2003:314966 CAPLUS
AN
DN
TI
      AML1/MTG8 oncogene suppression by small interfering RNAs supports myeloid
      differentiation of t(8;21)-positive leukemic cells
ΑU
      Heidenreich, Olaf; Krauter, Jurgen; Riehle, Heidemarie; Hadwiger, Philipp;
      John, Matthias; Heil, Gerhard; Vornlocher, Hans-Peter; Nordheim, Alfred
      Department of Molecular Biology, Institute for Cell Biology, University of
CS
      Tubingen, Tubingen, 72076, Germany Blood (2003), 101(8), 3157-3163 CODEN: BLOOAW; ISSN: 0006-4971
SO
PR
      American Society of Hematology
      Journal
DT
      English
LA
        39
RE.CNT
                 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
      ANSWER 5 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
      2003:277975 CAPLUS
AN
DN
      139:79491
      TI
      proteins and orphan nuclear receptor hepatocyte nuclear factor-4
```

```
Moustakas, Aristidis; Hadzopoulou-Cladaras, Margarita; Zannis, Vassilis
      I.; Kardassis, Dimitris
      Department of Basic Sciences, Foundation of Research and Technology of
CS
      Hellas, University of Crete Medical School and Institute of Molecular
      Biology and Biotechnology, Heraklion, GR-71110, Greece
     Molecular Biology of the Cell (2003), 14(3), 1279-1294
CODEN: MBCEEV; ISSN: 1059-1524
American Society for Cell Biology
SO
PB
      Journal
DT
      English
ΙΔ
RE.CNT 50
                 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 6 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2003:204939 CAPLUS
AN
DN
      139:30977
     Chromosomal region maintenance 1 (CRM1)-dependent nuclear export of Smad ubiquitin regulatory factor 1 (Smurf1) is essential for negative regulation of ***transforming*** ***growth*** ***factor*** -.
TI
      regulation of ***transforming***
        ***beta***
                       . signaling by Smad7
ΑU
      Tajima, Yoshitaka; Goto, Kouichiro; Yoshida, Minoru; Shinomiya, Kenichi;
     Sekimoto, Toshihiro; Yoneda, Yoshihiro; Miyazono, Kohei; Imamura, Takeshi
Department of Biochemistry, The Cancer Institute of the Japanese
CS
      Foundation for Cancer Research, 1-37-1 Kami-ikebukuro, Toshima-ku, Tokyo,
      170-8455, Japan
      Journal of Biological Chemistry (2003), 278(12), 10716-10721
SO
      CODEN: JBCHA3; ISSN: 0021-9258
PB
      American Society for Biochemistry and Molecular Biology
DT
      Journal
      English
LA
RE.CNT 28
                 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 7 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      2003:198116 CAPLUS
ΑN
      138:399539
DN
      Reconstitution of TGF-.beta. Sensitivity in the VACO-411 Human Colon
TT
     Carcinoma Line by Somatic Cell ***Fusion*** with MCF-7
Traicoff, June L.; Periyasamy, Sumudra; Brattain, Michael G.; Grady,
ΑU
      William; Casey, Graham
      Department of Molecular Biology and Microbiology, Case Western Reserve
CS
     University, Cleveland, OH, USA

Journal of Biomedical Science (Basel, Switzerland) (2003), 10(2), 253-259
50
      CODEN: JBCIEA; ISSN: 1021-7770
PB
      S. Karger AG
DT
      Journal
      English
LA
RE.CNT 15
                 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 8 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2003:125750 CAPLUS
AN
      138:364381
DN
TI
      An extended bipartite nuclear localization signal in Smad4 is required for
      its nuclear import and transcriptional activity
      Xiao, Zhan; Latek, Robert; Lodish, Harvey F.
ΑU
     Whitehead Institute for Biomedical Research, Cambridge, MA, 02142, USA
CS
     Oncogene (2003), 22(7), 1057-1069
SO
      CODEN: ONCNES; ISSN: 0950-9232
PB
      Nature Publishing Group
DT
      Journal
      English
LA
RE.CNT 21
                 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 9 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
ΑN
      2003:33503 CAPLUS
      138:332139
DN
TI
        ***Fusion***
                          proteins of retinoid receptors antagonize
      TGF-.beta.-induced growth inhibition of lung epithelial cells
     La, Ping; Morgan, Trish A.; Sykes, Stephen M.; Mao, Hua; Schnepp, Robert W.; Petersen, Clark D.; Hua, Xianxin Department of Cancer Biology, Abramson Family Cancer Research Institute, University of Pennsylvania, Philadelphia, PA, 19104-6160, USA
CS
```

Oncogene (2003), 22(2), 198-210

SO

```
PR
      Nature Publishing Group
DT
      Journal
      English
LA
RE.CNT 90
                 THERE ARE 90 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 10 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      2002:750454 CAPLUS
AN
      138:83786
DN
      TGF-.beta.3-induced chondroitin sulphate proteoglycan mediates palatal
TI
      shelf adhesion
ΑU
      Gato, A.; Martinez, M. L.; Tudela, C.; Alonso, I.; Moro, J. A.; Formoso,
      M. A.; Ferguson, M. W. J.; Martinez-Alvarez, C.
CS
      Departamento de Anatomia Humana, Facultad de Medicina, Universidad de
      Valladolid, Valladolid, 47005, Spain
S<sub>0</sub>
      Developmental Biology (Orlando, FL, United States) (2002), 250(2), 393-405
      CODEN: DEBIAO; ISSN: 0012-1606
PB
      Elsevier Science
      Journal
DT
      English
LA
RE.CNT 83
                 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 11 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2002:742821 CAPLUS
ΑN
DN
      138:71843
      Rhesus monocyte-derived dendritic cells modified to over-express
TT
     TGF-.beta.1 exhibit potent veto activity
Asiedu, Clement; Dong, Sai S.; Pereboev, Alexander; Wang, Weila; Navarro,
Jesus; Curiel, David T.; Thomas, Judith M.
Division of Transplant Immunology, Department of Surgery, University of
Alabama at Birmingham, Birmingham, AL, USA
CS
     Transplantation (2002), 74(5), 629-637 CODEN: TRPLAU; ISSN: 0041-1337
SO
      Lippincott Williams & Wilkins
PB
DT
      Journal
      English
LA
RE.CNT 38
                 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 12 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      2002:332053 CAPLUS
ΑN
      136:354178
DN
TI
      Novel therapeutic vaccine formulations comprising microparticles of weak
      immunogenic antigen and chitosan
IN
      Beier, Anne Mette; Gautam, Anand; Mouritsen, Soren
      Pharmexa A/S, Den.
PA
      PCT Int. Appl., 97 pp.
SO
      CODEN: PIXXD2
DT
      Patent
LA English FAN.CNT 1
      PATENT NO. KIND DATE
                                                    APPLICATION NO. DATE
PΙ
                         A2
      WO 2002034287
                                  20020502
                                                    WO 2001-DK705
                                                                       20011026
      WO 2002034287
                           Α3
                                  20030116
               AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
               CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, ES, FI,
               FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP,
               KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ
           RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
                BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
      AU 2002010407
                           Á5
                                  20020506
                                                    AU 2002-10407
PRAI DK 2000-1606
                                  20001027
     US 2000-245166P
                           Ρ
                                  20001103
     DK 2001-936
                           Α
                                  20010618
     WO 2001-DK705
                           W
                                  20011026
     ANSWER 13 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
      2002:218657 CAPLUS
AN
```

137:135411

DN

```
***factor*** -. ***beta***
                                         .1-stimulated Mv1Lu epithelial cells: Rad51
      as a target of TGF.beta.1-dependent regulation of DNA repair
ΑU
     Kanamoto, Takashi; Hellman, Ulf; Heldin, Carl-Henrik; Souchelnytskyi,
      Serhiy
CS
     Ludwig Institute for Cancer Research, Uppsala, SE-751 24, Swed.
     EMBO Journal (2002), 21(5), 1219-1230 CODEN: EMJODG; ISSN: 0261-4189
SO
PB
     Oxford University Press
      Journal
DT
     English
LA
RE.CNT 47
                THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 14 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     2001:868525 CAPLUS
ΑN
DN
     136:15216
ΤI
     Methods for identifying modulators of the interaction between LAP (latency
      associated peptide) and integrin .alpha.v.beta.3, and medical use thereof
IN
     Ludbrook, Steven; Barry, Simon; Horgan, Carmel; Miller, David
     Glaxo Group Limited, UK
PA
     PCT Int. Appl., 44 pp.
SO
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN. CNT 1
     PATENT NO.
                         KIND DATE
                                                APPLICATION NO. DATE
                                                ______
ΡI
     wo 2001090186
                               20011129
                         Α1
                                               wo 2001-GB2352
                                                                   20010525
             AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
              CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,
              RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ,
                                                           TR, TT, TZ, UA, UG, US,
          RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
               DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
               BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
                               20030226
     EP 1285001
                                                EP 2001-931955
                                                                   20010525
                          Α1
          R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, SI, LT, LV, FI, RO, MK, CY, AL, TR. 76315 A1 20030918 US 2003-
     us 2003176315
                                                US 2003-276947
                                                                   20030505
PRAI GB 2000-12991
                                20000526
                          Α
     GB 2001-286
                          Α
                               20010105
     WO 2001-GB2352
                               20010525
                          W
               THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 11
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 15 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     2001:808437 CAPLUS
ΑN
DN
     136:96576
TI
     Connective tissue growth factor is secreted through Golgi and is degraded
     in endosome
     Chen, Youjun; Segarini, Patricia; Raoufi, Fahimeh; Bradham, Douglass; Leask, Andrew
CS
     FibroGen, Inc., South San Francisco, CA, 94080, USA
     Experimental Cell Research (2001), 271(1), 109-117
SO
     CODEN: ECREAL; ISSN: 0014-4827
PB
     Academic Press
DT
     Journal
     English
LA
RE.CNT 39
               THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 16 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
ΑN
     2001:730469 CAPLUS
DN
     136:84625
TI
     Biological insights into TCR.gamma..delta.+ and TCR.alpha..beta.+
     intraepithelial lymphocytes provided by serial analysis of gene expression
AU
     Shires, John; Theodoridis, Efstathios; Hayday, Adrian C.
     Peter Gorer Department of Immunobiology Guy's, King's, Medical School King's College, University of London, London, SE1 9RT, UK
CS
SO
     Immunity (2001), 15(3), 419-434
     CODEN: IUNIEH; ISSN: 1074-7613
```

PB

Cell Press

```
English
RE.CNT 64
               THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 17 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     2001:582046 CAPLUS
AN
DN
     135:176996
TI
     Use of dendroaspin as vehicle for non-dendroaspin domains and
     pharmaceutical uses of chimeric proteinss
     Lu, Xinjie; Kakkar, Vijay Vir
IN
     Trigen Limited, UK
PA
     PCT Int. Appl., 39 pp.
SO
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN.CNT 1
     PATENT NO.
                        KIND DATE
                                               APPLICATION NO. DATE
PΙ
     wo 2001057210
                         A2
                               20010809
                                               WO 2001-GB439
                                                                  20010205
     wo 2001057210
                         Α3
                               20020214
              AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
              HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
              LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
              SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,
              ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
              DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG. 20102 A1 20020829 US 2001-779054 20010205
     US 2002120102
                                               EP 2001-949004
     EP 1252313
                         Α2
                               20021030
                                                                  20010205
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI GB 2000-2625 A 20000205
     WO 2001-GB439
                               20010205
     ANSWER 18 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
     2000:897036 CAPLUS
AΝ
DN
     134:51915
TI
     The transcriptional co-activator P/CAF potentiates TGF-.beta./smad
     signaling
     Itoh, Susumu; Ericsson, Johan; Nishikawa, Jun-Ichi; Heldin, Carl-Henrik;
ΑU
     Ten Dijke, Peter
     Division of Cellular Biochemistry, The Netherlands Cancer Institute,
CS
     Amsterdam, 1066 CX, Neth.
     Nucleic Acids Research (2000), 28(21), 4291-4298
SO
     CODEN: NARHAD; ISSN: 0305-1048
PB
     Oxford University Press
DT
     Journal
     English
LA
RE.CNT
         53
               THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 19 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
AN
     2000:856761 CAPLUS
DN
     134:145499
     Regulation of a multigenic invasion program by the transcription factor,
TT
     AP-1: re-expression of a down-regulated gene, TSC-36, inhibits invasion
AU
     Johnston, Imogen M. P.; Spence, Heather J.; Winnie, Joseph N.; McGarry,
     Lynn; Vass, J. Keith; Meagher, Liam; Stapleton, Genevieve; Ozanne,
     Bradford W.
     CRC Beatson Laboratories, Beatson Institute for Cancer Research, Glasgow,
CS
     G61 1BD, UK
     Oncogene (2000), 19(47),
                                5348-5358
SO
     CODEN: ONCNES; ISSN: 0950-9232
     Nature Publishing Group
PR
DT
     Journal
LA
     English
               THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
        95
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 20 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
L3
ΑN
     2000:735226
                   CAPLUS
```

Development of a Recombinant Bacterial Expression System for the Active

DN

TT

134:305914

```
Type II Receptor Ligand Binding Domain
ΑU
     Boesen, Christian C.; Motyka, Shawn A.; Patamawenu, Apisit; Sun, Peter D.
     Structural Biology Section, Laboratory of Immunogenetics, National
CS
     Institute of Allergy and Infectious Diseases, National Institutes of
     Health, Rockville, MD, 20852, USA
Protein Expression and Purification (2000), 20(1), 98-104
SO
     CODEN: PEXPEJ; ISSN: 1046-5928
     Academic Press
PB
DT
     Journal
     English
LA
RE.CNT 12
              THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 21 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     2000:695991 CAPLUS
AN
     133:305996
DN
     Role of Smad proteins and transcription factor Sp1 in p21Waf1/Cip1 regulation by ***transforming*** ***growth*** ***factor**
TI
                                                               ***factor*** -.
       ***beta***
     Pardali, Katerina; Kurisaki, Akira; Moren, Anita; ten Dijke, Peter; Kardassis, Dimitris; Moustakas, Aristidis
ΑU
     Ludwig Institute for Cancer Research, Uppsala, SE-751 24, Swed.
CS
S0
     Journal of Biological Chemistry (2000), 275(38), 29244-29256
     CODEN: JBCHA3; ISSN: 0021-9258
PB
     American Society for Biochemistry and Molecular Biology
DT
     Journal
     English
IΑ
RE.CNT 63
              THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 22 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     2000:241521 CAPLUS
ΑN
     132:289231
DN
                      proteins of ***functional***

19*** ***growth*** ***fac
       ***Fusion***
                                                          domains of the
TI
                                                 ***factor*** . ***beta***
       ***transforming***
     family of proteins and their prepn., biol. activity and uses
     Oppermann, Hermann; Tai, Mei-Sheng; McCartney, John
IN
     Stryker Corporation, USA
PA
50
     PCT Int. Appl., 162 pp.
     CODEN: PIXXD2
DT
     Patent
     English
LA
FAN.CNT 3
     PATENT NO.
                       KIND DATE
                                             APPLICATION NO. DATE
PΙ
     wo 2000020607
                       A2
                             20000413
                                             wo 1999-US23371 19991007
     wo 2000020607
                       Α3
                             20000706
             AU, CA, JP
         RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
              PT, SE
     CA 2344974
                        AA
                             20000413
                                             CA 1999-2344974 19991007
     EP 1117804
                        A2
                             20010725
                                             EP 1999-954771
                                                               19991007
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
     JP 2002526115
                        T2
                             20020820
                                             JP 2000-574702
                                                               19991007
PRAI US 1998-103418P
                        Ρ
                             19981007
     US 1999-374958
                             19990816
                        Α
     WO 1999-US23371
                        W
                             19991007
L3
     ANSWER 23 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
     2000:241494 CAPLUS
DN
     132:289230
       ***Fusion***
                       proteins of
                                    ***functional***
TI
                                                         domains of the
       family of proteins and their preparation, biological activity and uses
     Oppermann, Hermann; Tai, Mei-Sheng; McCartney, John
IN
PA
     Stryker Corporation, USA
SO
     PCT Int. Appl., 149 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN.CNT 3
     PATENT NO.
                       KIND
                                             APPLICATION NO.
                             DATE
                                                               DATE
     wo 2000020591
                                             WO 1999-US23370
PΙ
                             20000413
                                                               19991007
                        Α2
```

```
AU, CA, JP
          RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
              PT, SE
      CA 2345287
                               20000413
                                               CA 1999-2345287
                                                                 19991007
      EP 1117795
                         Α2
                               20010725
                                               EP 1999-954770
                                                                 19991007
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, FI
      JP 2002526111
                         T2
                               20020820
                                               JP 2000-574686
                                                                 19991007
PRAI US 1998-103418P
                         Ρ
                               19981007
     US 1999-374936
                               19990816
                         Α
     WO 1999-US23370
                         W
                               19991007
L3
     ANSWER 24 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
AN
      2000:240985 CAPLUS
     132:292701
DN
     Novel methods for therapeutic vaccination
TI
IN
     Steinaa, Lucilla; Mouritsen, Soren; Nielsen, Klaus Gregorious; Haaning,
      Jesper; Leach, Dana; Dalum, Iben; Gautam, Anand; Birk, Peter; Karlsson,
      Gunilla
PA
     M & E Biotech A/S, Den.
     PCT Int. Appl., 220 pp.
SO
     CODEN: PIXXD2
DT
      Patent
     English
LA
FAN.CNT 1
      PATENT NO.
                        KIND
                              DATE
                                               APPLICATION NO.
                                                                 DATE
                        ----
                              -----
                                              WO 1999-DK525
PΙ
     wo 2000020027
                        A2
                               20000413
                                                                 19991005
     wo 2000020027
                        Α3
                              20001012
              AE, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
              LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO,
              RU, SD, SE, SG, SI, SK, SK, SL,
                                                 TJ, TM, TR, TT, UA, UG, US, UZ,
              VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ,
                                                                  TM
          RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
              DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
              CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     CA 2345817
                         AA
                               20000413
                                              CA 1999-2345817
                                                                 19991005
     AU 9958510
                         Α1
                               20000426
                                               AU 1999-58510
                                                                 19991005
     AU 751709
                         В2
                               20020822
     EP 1117421
                                               EP 1999-945967
                         Α2
                              20010725
                                                                 19991005
              AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, MC, IE, SI,
              LT, LV, FI, RO
     JP 2002526419
                         Ť2
                              20020820
                                               JP 2000-573386
                                                                 19991005
     EE 200100203
                               20021015
                         Α
                                               EE 2001-203
                                                                 19991005
     NO 2001001586
                              20010531
                                               NO 2001-1586
                                                                 20010328
     ZA 2001002603
                              20020930
                         Α
                                               ZA 2001-2603
                                                                 20010329
                              20020630
     HR 2001000319
                         A1
                                               HR 2001-319
                                                                 20010504
PRAI DK 1998-1261
                              19981005
                         Α
     US 1998-105011P
                         Р
                               19981020
     WO 1999-DK525
                         W
                              19991005
L3
     ANSWER 25 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1999:673041 CAPLUS
ΑN
DN
     131:282025
TI
     Improved methods for making hormone heterodimers for therapeutic and
     disagnostic purposes
IN
     Moyle, William R.
PA
     University of Medicine & Dentistry of New Jersey, USA
so
     PCT Int. Appl., 73 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN.CNT 1
     PATENT NO.
                        KIND
                              DATE
                                              APPLICATION NO.
                                                                 DATE
PΙ
     wo 9953065
                        Α1
                              19991021
                                              wo 1999-us8018
                                                                 19990413
             AU, CA, JP
         RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
              PT, SE
     us 6486303
                                               US 1998-59625
                                                                 19980414
                         В1
                              20021126
     AU 9935561
                         A1
                              19991101
                                              AU 1999-35561
                                                                 19990413
PRAI US 1998-59625
                         Α
                              19980414
```

19990413

W

wo 1999-US8018

ALL CITATIONS AVAILABLE IN THE RE FORMAT

```
L3
     ANSWER 26 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     1999:672013 CAPLUS
AN
DN
      132:31626
TI
     c-Jun transactivates the promoter of the human p21WAF1/Cip1 gene by acting
     as a superactivator of the ubiquitous transcription factor Sp1
     Kardassis, Dimitris; Papakosta, Paraskevi; Pardali, Katerina; Moustakas,
ΑU
CS
     Department of Basic Sciences, University of Crete Medical School and
     Institute of Molecular Biology and Biotechnology, Foundation of Research
     and Technology of Hellas, Crete, GR-71110, Greece
SO
     Journal of Biological Chemistry (1999), 274(41), 29572-29581
     CODEN: JBCHA3; ISSN: 0021-9258
PB
     American Society for Biochemistry and Molecular Biology
DT
     Journal
     English
LA
RE.CNT 71
               THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 27 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     1999:104567 CAPLUS
AN
     130:291720
DN
        ***Functional***
                            association of TGF-.beta. receptor II with cyclin B
TI
     Liu, Jin Hong; Wei, Sheng; Burnette, Pearlie K.; Gamero, Ana M.; Hutton, Michael; Djeu, Julie Y.
ΑU
     Immunology Program, H Lee Moffitt Cancer Center and Research Institute,
     Department of Biochemistry and Molecular Biology, University of South Florida, Tampa, FL, 33612, USA Oncogene (1999), 18(1), 269-275
SO
     CODEN: ONCNES; ISSN: 0950-9232
PB
     Stockton Press
DT
     Journal
     English
LA
RE.CNT 39
               THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 28 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
     1998:805570 CAPLUS
     130:91225
DN
TI
     SMAD3/4-dependent transcriptional activation of the human type VII
     collagen gene (COL7A1) promoter by ***transforming***
***factor*** . ***beta***
                                                                      ***arowth***
ΑU
     Vindevoghel, Laurence; Lechleider, Robert J.; Kon, Atsushi; De Caestecker,
     Mark P.; Uitto, Jouni; Roberts, Anita B.; Mauviel, Alain
CS
     Department of Dermatology and Cutaneous Biology, Jefferson Medical
     College, Jefferson Institute of Molecular Medicine, Thomas Jefferson
     University, Philadelphia, PA, 19107, USA
Proceedings of the National Academy of Sciences of the United States of
America (1998), 95(25), 14769-14774
CODEN: PNASA6; ISSN: 0027-8424
SO
     National Academy of Sciences
PB
DT
     Journal
LA
     English
RE.CNT 39
               THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 29 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
AN
     1998:803928 CAPLUS
DN
     130:62035
                     ***functional***
TI
     sequence and
                                          expression and therapeutic applications
     for human chordin
IN
     Lavallie, Edward R.; Racie, Lisa A.; Derobertis, Edward M.
     Genetics Institute, Inc., USA
PA
SO
     U.S., 22 pp., Cont.-in-part of U.S. 5,679,783.
     CODEN: USXXAM
DT
     Patent
     English
LA
FAN.CNT 3
     PATENT NO.
                       KIND DATE
                                              APPLICATION NO. DATE
PΙ
     us 5846770
                              19981208
                                              US 1996-749169
                                                                 19961114
     us 5679783
                       Α
                              19971021
                                              us 1994-343760
                                                                 19941122
                       A1
     wo 9821335
                              19980522
                                              wo 1997-US18151 19971007
```

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,

```
LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR,
               GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA,
               GN, ML, MR, NE, SN, TD, TG
      AU 9748960
                         Α1
                                19980603
                                                  AU 1997-48960
                                                                      19971007
      US 5986056
                          Α
                                19991116
                                                  US 1998-130032
                                                                      19980804
PRAI US 1994-343760
                                19941122
      US 1996-749169
                                19961114
      WO 1997-US18151
                                19971007
         56
                THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 30 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      1998:790670 CAPLUS
ΑN
DN
      130:34762
     Smad2 mutants and Smad-binding Smad2 peptides and methods for inhibiting ***transforming*** ***growth*** ***factor*** ***beta***
TI
      signal transduction
      Souchelnytskyi, Serhiy; Tamaki, Kiyoshi; Engstrom, Ulla; Wernstedt, Christer; Piek, Esther; Ten, Dijke Peter; Henrik, Carl
IN
РΔ
      Ludwig Institute for Cancer Research, USA
SO
      PCT Int. Appl., 83 pp.
      CODEN: PIXXD2
DT
      Patent
LA
      English
FAN.CNT 1
                         KIND DATE
      PATENT NO.
                                                  APPLICATION NO. DATE
PΙ
      wo 9853066
                         Α1
                                19981126
                                                 wo 1998-US10271 19980520
               AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,
               KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
               NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR,
               UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
               FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
               CM, GA, GN, ML, MR, NE, SN, TD, TG
                                19981211
      AU 9875812
                          Α1
                                                 AU 1998-75812
                                                                      19980520
      AU 741242
                          B2
                                20011129
      EP 983356
                                20000308
                                                  EP 1998-923545
                                                                      19980520
                          Α1
               AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
      us 6103869
                                20000815
                                                  US 1998-82039
                                                                      19980520
      JP 2001507239
                          T2
                                20010605
                                                  JP 1998-550549
                                                                      19980520
      us 6368829
                          в1
                                20020409
                                                  us 2000-552138
                                                                      20000419
      US 2002146774
                          Α1
                                20021010
                                                  US 2002-119099
                                                                      20020409
PRAI US 1997-47807P
                          Р
                                19970520
      US 1998-81313P
                                19980410
                          Р
                                19980520
      US 1998-82039
                          Α3
         1998-US10271
                          W
                                19980520
     US 2000-552138
                          Α3
                                20000419
RE.CNT 9
                THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
     ANSWER 31 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
      1998:685114 CAPLUS
DN
      129:313128
TI
     Characterizing a cellular response to a stimulus using a lumiphore
      genetically modified with a signal pathway component
ΙN
      Thastrup, Ole; Petersen Bjorn, Sara; Tullin, Soren; Kasper, Almholt;
      Scudder, Kurt
PΑ
     Novo Nordisk A/s, Den.
SO
     PCT Int. Appl., 327 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN.CNT 1
      PATENT NO.
                         KIND
                               DATE
                                                 APPLICATION NO.
                                                                     DATE
                         A2
ΡI
     wo 9845704
                                19981015
                                                 WO 1998-DK145
                                                                     19980407
                                19990422
     wo 9845704
                          Α3
              AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,
```

```
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
               FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
               CM, GA, GN, ML, MR, NE, SN, TD, TG
      AU 9868209
                                                                      19980407
                                 19981030
                                                  AU 1998-68209
                           Α1
      EP 986753
                                 20000322
                                                  EP 1998-913541
                           Α2
                                                                      19980407
      EP 986753
                           В1
                                20020327
               AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, LT, LV, FI
      JP 2001522454
                           T2
                                 20011113
                                                  JP 1998-542276
                                                                      19980407
                                                  AT 1998-913541
      AT 215227
                                 20020415
                                                                      19980407
                           Ε
      EP 1199564
                           A2
                                 20020424
                                                  EP 2001-204477
                                                                      19980407
      EP 1199564
                           Α3
                                 20020508
              AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
               IE, SI, LT, LV, FI, RO, MK, CY, AL
      ES 2173573
                           T3
                                 20021016
                                                  ES 1998-913541
                                                                      19980407
                                                  US 1999-417197
                                 20030211
      US 6518021
                                                                      19991007
                           В1
      us 2003082564
                                 20030501
                           Α1
                                                  US 2002-72036
                                                                      20020205
PRAI DK 1997-392
                                 19970407
                           Α
      EP 1998-913541
                           Α3
                                 19980407
                                 19980407
      WO 1998-DK145
                           W
      US 1999-417197
                           A3
                                 19991007
L3
      ANSWER 32 OF 40
                         CAPLUS COPYRIGHT 2003 ACS on STN
      1998:378471 CAPLUS
ΑN
DN
      129:132071
TI
      Regulation of the human p21/WAF1/Cip1 promoter in hepatic cells by
     ***functional*** interactions between Sp1 and Smad family members Moustakas, Aristidis; Kardassis, Dimitris Division of Basic Sciences, School of Medicine, University of Crete,
CS
      Crete, 71110, Greece
Proceedings of the National Academy of Sciences of the United States of
S<sub>0</sub>
      America (1998), 95(12), 6733-6738
      CODEN: PNASA6; ISSN: 0027-8424
PB
      National Academy of Sciences
DΤ
      Journal
      English
LA
RE.CNT
         39
                THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 33 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
      1998:32752
AN
                   CAPLUS
      128:178293
DN
TI
      The DAF-3 Smad protein antagonizes TGF-.beta.-related receptor signaling
      in the Caenorhabditis elegans dauer pathway
      Patterson, Garth I.; Koweek, Allison; Wong, Arthur; Liu, Yanxia; Ruvkun,
CS
      Department of Molecular, Harvard Medical School, Boston, MA, 02114, USA
     Genes & Development (1997), 11(20), 2679-2690
CODEN: GEDEEP; ISSN: 0890-9369
S0
PR
      Cold Spring Harbor Laboratory Press
DT
      Journal
      English
LA
RE.CNT 49
                THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3
      ANSWER 34 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
      1997:732166 CAPLUS
ΑN
DN
      128:10885
TI
      Increasing the level of expression of a foreign gene in eukaryotes using a
      nuclear retention signal and nuclear export factor
      Sedlacek, Hans Harald; Muller, Rolf; Luhrmann, Reinhard
IN
PA
      Hoechst Aktiengesellschaft, Germany
S<sub>0</sub>
     Eur. Pat. Appl., 41 pp.
      CODEN: EPXXDW
DT
      Patent
LA
      German
FAN.CNT 1
     PATENT NO.
                         KIND
                                DATE
                                                  APPLICATION NO.
                                                                      DATE
ΡI
     EP 805209
                          A2
                                19971105
                                                  EP 1997-106531
                                                                      19970421
      EP 805209
                          Α3
                                19980422
          R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI
L9617851 A1 19971113 DE 1996-19617851 19960503
```

DE 19617851

```
19970501
     AU 9719982
                                             AU 1997-19982
                        Α1
                              19971106
     AU 716178
                        в2
                              20000217
                              19971103
     CA 2204332
                                             CA 1997-2204332
                                                               19970502
                        AA
     ZA 9703802
                             19971103
                                             ZA 1997-3802
                                                                19970502
                        Α
     US 6235526
                        в1
                             20010522
                                             us 1997-850744
                                                                19970502
     JP 11000167
                        Α2
                              19990106
                                              JP 1997-115947
                                                                19970506
PRAI DE 1996-19617851 A
                             19960503
     ANSWER 35 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN 1997:567057 CAPLUS
L3
AN
     127:243372
DN
     Transforming growth factor (TGF-.beta.)-specific signaling by chimeric
TI
     TGF-.beta. type II receptor with intracellular domain of activin type IIB
     receptor
     Persson, Urban; Souchelnytskyi, Serhiy; Franzen, Petra; Miyazono, Kohei;
ΑU
     Ten Dijke, Peter; Heldin, Carl-Henrik
     Ludwig Institute for Cancer Research, Uppsala, S-751 24, Swed.
CS
     Journal of Biological Chemistry (1997), 272(34), 21187-21194
50
     CODEN: JBCHA3; ISSN: 0021-9258
PB
     American Society for Biochemistry and Molecular Biology
DT
     Journal
     English
LA
L3
     ANSWER 36 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1994:694379 CAPLUS
AN
DN
     121:294379
TI
     A monomeric derivative of the cellular transcription factor CREB functions
     as a constitutive activator
     Krajewski, Wladyslaw; Lee, Kevin A. W.
AU
     Imp. Cancer Res. Fund, Clare Hall Lab., South Mimms, Hertfordshire, EN6
CS
     3LD, UK
     Molecular and Cellular Biology (1994), 14(11), 7204-10
SO
     CODEN: MCEBD4; ISSN: 0270-7306
     American Society for Microbiology
PR
DT
     Journal
     English
LA
L3
     ANSWER 37 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1994:549708 CAPLUS
AN
DN
     121:149708
TI
     PML/RAR.alpha.+ U937 mutant and NB4 cell lines: retinoic acid restores the
     monocytic differentiation response to vitamin D3
ΑU
     Testa, Ugo; Grignani, Francesco; Barberi, Tiziano; Fagioli, Marta;
     Masciulli, Rosalba; Ferrucci, Pier Francesco; Seripa, Davide; Camagna,
     Antonio; Alcalay, Myrian; et al.
     Department of Hematology and Oncology, Istituto Superiore di Sanita, Rome,
CS
     Italy
SO
     Cancer Research (1994), 54(16), 4508-15
     CODEN: CNREA8; ISSN: 0008-5472
DT
     Journal
     English
LA
L3
     ANSWER 38 OF 40 CAPLUS COPYRIGHT 2003 ACS on STN
     1993:552114 CAPLUS
AN
DN
     119:152114
     Inhibitors of cell regulatory factors and methods for preventing or
TI
     reducing scarring
     Ruoslahti, Erkki I.; Longaker, Michael T.; Whitby, David J.; Harper, John
IN
     R.; Pierschbacher, Michael D.; Border, Wayne A.
     La Jolla Cancer Research Foundation, USA; University of California;
PA
     University of Utah
SO
     PCT Int. Appl., 73 pp.
     CODEN: PIXXD2
DT
     Patent
ΙΑ
     English
FAN.CNT 6
                       KIND DATE
     PATENT NO.
                                             APPLICATION NO. DATE
     wo 9309800
PI
                       Α1
                             19930527
                                             wo 1992-US9871
                                                               19921113
            AU, BB, BG, BR, CA, CS, FI, HU, JP, KP, KR, LK, MG, MN, MW, NO,
             PL, RO, RU, SD, US
         RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, SN, TD, TG
9331385 A1 19930615 AU 1993-31385 19921113
```

AU 9331385 AU 673506

В2

19961114

```
EP 667784
                         в1
                              20030305
         R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, SE
     EP 1230929
                        A1
                              20020814
                                              EP 2002-10251
                                                                 19921113
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, IE
     AT 233568
                                              ÁT 1992-925260
                        Ε
                              20030315
                                                                 19921113
     ES 2188585
                        Т3
                                              ES 1992-925260
                              20030701
                                                                 19921113
     FI 9402244
                                              FI 1994-2244
                                                                 19940513
                              19940706
                         Α
     NO 9401821
                                                                 19940513
                        Α
                              19940714
                                              NO 1994-1821
                                              US 1994-303238
US 1995-442063
     US 5654270
                              19970805
                                                                 19940908
                         Α
     us 5705609
                              19980106
                                                                 19950516
                                              US 1995-458834
     US 6277812
                         В1
                              20010821
                                                                 19950602
     US 2003032591
                                              US 2001-935216
                         Α1
                              20030213
                                                                 20010821
PRAI US 1991-792192
                              19911114
                         Α
     US 1992-882345
                         A2
                              19920513
     US 1988-212702
                         В2
                              19880628
     US 1990-467888
                         В2
                              19900122
     US 1992-865652
                         в1
                              19920403
     EP 1992-925260
                         Α3
                              19921113
     WO 1992-US9871
                              19921113
                         Α
     US 1992-978931
                         В1
                              19921117
     US 1994-303238
                         Α1
                              19940908
     US 1995-458834
                              19950602
                         Α1
L3
     ANSWER 39 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
     1992:505095 CAPLUS
AN
DN
     117:105095
     Regulation of murine embryonic epithelial cell differentiation by
TI
                                ***growth***
                                                                   . ***beta***
        ***transforming***
                                                  ***factors***
     Gehris, Amy L.; Green, Robert M.
Jefferson Med. Coll., Thomas Jefferson Univ., Philadelpia, PA, 19107, USA
Differentiation (Berlin, Germany) (1992), 49(3), 167-73
AU
CS
SO
     CODEN: DFFNAW; ISSN: 0301-4681
DT
     Journal
     English
LA
L3
     ANSWER 40 OF 40 CAPLUS COPYRIGHT 2003 ACS ON STN
AN
     1990:230385 CAPLUS
     112:230385
DN
ΤI
       ***Functional***
                          receptors for ***transforming***
                                                                      ***growth***
       ***factor*** -. ***beta*** . are retained by biochemically
     differentiated C2 myocytes in growth factor-deficient medium containing
     EGTA but down-regulated during terminal differentiation
     Hu, Jing Shan; Olson, Eric N.
M. D. Anderson Cancer Cent., Univ. Texas, Houston, TX, 77030, USA
ΑU
CS
     Journal of Biological Chemistry (1990), 265(14), 7914-19
SO
     CODEN: JBCHA3; ISSN: 0021-9258
DT
     Journal
     English
LA
=> D L4 1-27
L4
     ANSWER 1 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
ΑN
     2003:696617
                  CAPLUS
DN
     139:225485
     Methods for cloning, synthesis and purification of human growth hormone
TI
     and granulocyte colony stimulating factor in plants
IN
     Russell, Douglas A.; Schlittler, Michael
PA
SO
     U.S. Pat. Appl. Publ., 53 pp., Cont.-in-part of U.S. Ser. No. 316,847,
     abandoned.
     CODEN: USXXCO
DT
     Patent
LA
     English
FAN.CNT 3
                       KIND DATE
     PATENT NO.
                                              APPLICATION NO.
                                                                 DATE
PI
     US 2003167531
                         Α1
                              20030904
                                              US 2001-824200
                                                                 20010403
                              20020502
     US 2002053094
                         Α1
                                              us 1998-113244
                                                                 19980710
                         В2
                              20030128
     US 6512162
                                              US 2002-103516
     US 2003033636
                         Α1
                              20030213
                                                                 20020320
                              19980710
PRAI US 1998-113244
                         A2
     US 1999-316847
                         в2
                              19990521
                              20000403
```

US 2000-194217P

Р

```
AN
      2003:336102 CAPLUS
DN
      139:63517
ΤI
      Growth Factor-Binding Sequence in Human .alpha.2-Macroglobulin Targets the
      Receptor-Binding Site in ***

***Factor*** -. ***beta***
                                      ***Transforming***
                                                                  ***Growth***
      Arandjelovic, Sanja; Freed, Tiffany A.; Gonias, Steven L.
ΑU
      Departments of Pathology and Biochemistry and Molecular Genetics,
CS
     Charlottesville, VA, 22908, USA
Biochemistry (2003), 42(20), 6121-6127
CODEN: BICHAW; ISSN: 0006-2960
PB
      American Chemical Society
      Journal
DT
      English
LA
RE.CNT
        59
                THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
      ANSWER 3 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
      2002:864122 CAPLUS
AN
DN
      138:71370
TI
      Converting nonhuman primate dendritic cells into potent antigen-specific
      cellular immunosuppressants by genetic modification
     Asiedu, Clement; Pereboev, Alexander; Curiel, David T.; Dong, Sai Sai;
ΑU
     Hutchings, Anne; Thomas, Judith M.
     Division of Transplantation Immunobiology, Department of Surgery,
CS
      University of Alabama at Birmingham, USĀ
      Immunologic Research (2002), 26(1-3), 297-302
SO
      CODEN: IMRSEB; ISSN: 0257-277X
PB
     Humana Press Inc.
      Journal; General Review
DT
LA
      English
RE.CNT 30
                THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 4 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      2002:742821 CAPLUS
AN
DN
      138:71843
      Rhesus monocyte-derived dendritic cells modified to over-express
TI
      TGF-.beta.1 exhibit potent veto activity
     Asiedu, Clement; Dong, Sai S.; Pereboev, Alexander; Wang, Weila; Navarro, Jesus; Curiel, David T.; Thomas, Judith M.
ΑU
CS
     Division of Transplant Immunology, Department of Surgery, University of
     Alabama at Birmingham, Birmingham, AL, USA Transplantation (2002), 74(5), 629-637
SO
     CODEN: TRPLAU; ISSN: 0041-1337
PB
      Lippincott Williams & Wilkins
      Journal
DT
LA
      English
RE.CNT 38
                THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 5 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
AN
      2001:748023 CAPLUS
      135:314414
DN
     Expression and purification of bioactive, authentic human growth hormone and granulocyte colony stimulating factor in plants
TI
      Russell, Douglas; Schlittler, Michael
IN
     Monsanto Technology Llc, USA
PA
SO
      PCT Int. Appl., 97 pp.
      CODEN: PIXXD2
DT
      Patent
     English
LA
FAN.CNT 3
      PATENT NO.
                          KIND
                                 DATE
                                                   APPLICATION NO. DATE
                          ____
PΙ
                           A2
                                 20011011
     wo 2001075132
                                                   wo 2001-us10765 20010403
     wo 2001075132
                           Α3
                                 20020606
               AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
               CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
               HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
               LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
          SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
```

```
AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
-194217P P 20000403
PRAI US 2000-194217P
      WO 2001-US10765
                                  20010403
                           W
L4
      ANSWER 6 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      2001:125225 CAPLUS
AN
      134:309568
DN
      Blockade of TGF-.beta. signaling in T cells prevents the development of
TI
      experimental glomerulonephritis
      Kanamaru, Yutaka; Nakao, Atsuhito; Mamura, Mizuko; Suzuki, Yusuke; Shirato, Isao; Okumura, Ko; Tomino, Yasuhiko; Ra, Chisei
Allergy Research Center, Division of Nephrology, School of Medicine,
CS
      Juntendo University, Tokyo, 113-8421, Japan Journal of Immunology (2001), 166(4), 2818-2823
50
      CODEN: JOIMA3; ISSN: 0022-1767
PR
      American Association of Immunologists
      Journal
DT
      English
LA
RE.CNT
        31
                 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 7 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      2000:856739 CAPLUS
AN
      134:37538
DN
TI
      A 16-amino acid peptide from human .alpha.2-macroglobulin binds
         ***transforming*** ***growth***
                                                        ***factor*** -. ***beta***
      and platelet-derived growth factor-BB
      Webb, Donna J.; Roadcap, David W.; Dhakephalkar, Anita; Gonias, Steven L. Departments of Pathology, Biochemistry, University of Virginia School of Medicine, Charlottesville, VA, 22908, USA Protein Science (2000), 9(10), 1986-1992
ΔIJ
CS
S0
      CODEN: PRCIEI; ISSN: 0961-8368
PB
      Cambridge University Press
      Journal
DT
      English
LA
RE.CNT 35
                 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
                 ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 8 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
AN
      1999:392621 CAPLUS
DN
      131:54753
      Expression of
                        ***fusion***
TI
                                           polypeptides transported out of the
      cytoplasm without leader sequences
      Mascarenhas, Desmond; Zhang, Yang; Olson, Pamela S.; Olsen, David R.;
IN
      Cohen, Pedro A.; Nguyen, Kimyen B.
PA
      Celtrix Pharmaceuticals, Inc., USA
      U.S., 80 pp., Cont.-in-part of U.S. 5,629,172.
S0
      CODEN: USXXAM
DT
      Patent
      English
LA
FAN.CNT 3
      PATENT NO.
                          KIND
                                 DATE
                                                   APPLICATION NO.
                                                                       DATE
PΙ
      US 5914254
                                 19990622
                                                   US 1997-854811
                           Α
                                                                        19970512
      us 5563046
                                                   US 1993-100744
                           Α
                                 19961008
                                                                        19930802
      US 5629172
                                                   US 1994-284784
                           Α
                                 19970513
                                                                       19940802
PRAI US 1993-100744
                          A2
                                 19930802
      US 1994-284784
                           A2
                                 19940802
                THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 58
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 9 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      1999:274814
AN
                    CAPLUS
DN
      131:57268
TI
      TGF-.beta.1 in liver fibrosis: an inducible transgenic mouse model to
      study liver fibrogenesis
      Kanzler, Stephan; Lohse, Ansgar W.; Keil, Andrea; Henninger, Jurgen;
      Dienes, Hans P.; Schirmacher, Peter; Rose-John, Stefan; Buschenfelde, Karl
      H. Meyer Zum; Blessing, Manfred
      Boehringer Ingelheim Research Group, and 2First Department of Medicine,
CS
      University of Mainz, Mainz, 55101, Germany
American Journal of Physiology (1999), 276(4, Pt. 1), G1059-G1068
```

CODEN: AJPHAP; ISSN: 0002-9513 American Physiological Society

PB

```
English
RE.CNT 62
                THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
      ANSWER 10 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
      1998:352861 CAPLUS
AN
DN
      129:50102
      Nucleotide and protein sequences of liver activin/inhibin and and their
TI
     therapeutic activities
Bonadio, Jeffrey; Fang, Jianming
Regents of the University of Michigan, USA
IN
PA
      PCT Int. Appl., 143 pp.
50
      CODEN: PIXXD2
DT
      Patent
      English
LA
FAN.CNT 1
      PATENT NO.
                         KIND DATE
                                                 APPLICATION NO. DATE
                                19980528
                                                 wo 1997-us20882 19971120
     wo 9822492
                         Α1
PΙ
          W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, GE, GH, HU, ID, IL, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR,
               GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA,
               GN, ML, MR, NE, SN, TD, TG
     AU 9853567
                                19980610
                         A1
                                                 AU 1998-53567
                                                                    19971120
      AU 743792
                          B2
                                20020207
      EP 960118
                                                                    19971120
              AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
                          Α1
                                19991201
                                                 EP 1997-950609
      JP 2001505420
                                20010424
                          T2
                                                 JP 1998-523766
                                                                    19971120
PRAI US 1996-752919
                         Α
                                19961120
     WO 1997-US20882
                          W
                                19971120
               THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 3
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L4
     ANSWER 11 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      1997:544772 CAPLUS
ΑN
      127:243767
DN
      Capture and expansion of bone marrow-derived mesenchymal progenitor cells
TI
     with a ***transforming*** ***growth*** ***factor***
      ***beta*** .1-von Willebrand's factor ***fusion**
retrovirus-mediated delivery of coagulation factor IX
                                                     ***fusion***
                                                                       protein for
ΑU
     Gordon, Erlinda M.; Skotzko, Michael; Kundu, Ramendra Krishna; Han, Bo;
     Andrades, Jose; Nimni, Marcel; Anderson, W. French; Hall, Frederick L.
     Gene Therapy Laboratories, Childrens Hospital Los Angeles, Los Angeles,
CS
     CA, 90033, USA
SO
     Human Gene Therapy (1997), 8(11), 1385-1394
     CODEN: HGTHE3; ISSN: 1043-0342
PB
     Liebert
DT
      Journal
     English
LA
     ANSWER 12 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
     1997:474561 CAPLUS
AN
DN
      127:131561
        ***Transforming***
                                 ***growth***
TI
                                                     ***factor*** -. ***beta***
     regulates transdifferentiation of medial edge epithelium during palatal
        ***fusion*** and associated degradation of the basement membrane
ΑU
     Kaartinen, Vesa; Cui, Xiao-Mei; Heisterkamp, Nora; Groffen, John; Shuler.
     Charles F.
CS
     Department of Pathology, Childrens Hospital Los Angeles Research
     Institute, Los Angeles, CA, USA
Developmental Dynamics (1997), 209(3), 255-260
SO
     CODEN: DEDYEI; ISSN: 1058-8388
PB
     Wiley-Liss
DT
     Journal
LA
     English
L4
     ANSWER 13 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1997:341952 CAPLUS
ΑN
DN
     126:313187
```

Recombinant expression of protein of interest as ***fusion***

with interleukin-1-like protein or leader-peptide-deleted-translocating

TI

```
ΙN
     Mascarenhas, Desmond; Zhang, Yang; Olson, Pamela S.; Olsen, David R.;
     Cohen, Pedro A.
     Celtrix Pharmaceuticals, Inc., USA
U.S., 77 pp., Cont.-in-part of U.S. Ser. No. 100,744.
PA
SO
     CODEN: USXXAM
DT
     Patent
     English
LA
FAN.CNT 3
     PATENT NO.
                        KIND DATE
                                                APPLICATION NO. DATE
                               19970513
PΙ
     us 5629172
                         Α
                                                US 1994-284784
                                                                   19940802
     us 5563046
                                                US 1993-100744
                               19961008
                         Α
                                                                   19930802
                               19950209
     CA 2168429
                                                CA 1994-2168429 19940802
                         AA
     CA 2168429
                         C
                               20010605
     us 5830706
                               19981103
                                                us 1995-460915
                         Α
                                                                   19950605
     US 5914254
                               19990622
                                                US 1997-854811
                                                                   19970512
PRAI US 1993-100744
                         A2
                               19930802
     US 1994-284784
                               19940802
                         A2
L4
     ANSWER 14 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1997:182887
AN
                   CAPLUS
DN
     126:236690
TI
     Type I collagen combined with a recombinant TGF-.beta. serves as a
     scaffold for mesenchymal stem cells
     Andrades, Jose A.; Nimni, Marcel E.; Han, Bo; Ertl, Delia C.; Hall,
     Frederick L.; Becerra, Jose
Department of Cell Biology and Genetics, Faculty of Sciences, University
CS
     of Malaga, Malaga, 29071, Spain
SO
     International Journal of Developmental Biology (1996), (Suppl. 1,
     Proceedings of the First Congress of the Spanish Society of Developmental
     Biology, 1996), 107s-108s
CODEN: IJDBE5; ISSN: 0214-6282
University of the Basque Country Press
PB
DT
     Journal
     English
I A
L4
     ANSWER 15 OF 27 CAPLUS COPYRIGHT 2003 ACS ON STN
     1997:182767 CAPLUS
ΑN
DN
     126:272449
     Latent ***transforming***
TI
                                        ***growth***
                                                            ***factor*** -.
        ***beta*** . binding protein domains involved in activation and
     transglutaminase-dependent crosslinking of latent ***growth*** ***factor*** -. ***beta***.
                                                               ***transforming***
     Nunes, Irene; Gleizes, Pierre-Emmanuel; Metz, Christine N.; Rifkin, Daniel
ΑU
CS
     Department of Cell Biology, Kaplan Cancer Center, New York University
     Medical Center, New York, NY, 10016, USA
Journal of Cell Biology (1997), 136(5), 1151-1163
SO
     CODEN: JCLBA3; ISSN: 0021-9525
PB
     Rockefeller University Press
DT
     Journal
lΑ
     English
L4
     ANSWER 16 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1995:479799 CAPLUS
AN
     122:236790
DN
     Hepatic expression of ***mature***
                                                  ***transforming***
TI
        ***growth*** ***factor***
                                              ***beta*** .1 in transgenic mice
     results in multiple tissue lesions
     Sanderson, Nancy; Factor, Valentina; Nagy, Peter; Kopp, Jeffrey; Kondaiah,
ΑU
     Paturu; Wakefield, Lalage; Roberts, Anita B.; Sporn, Michael B.;
     Thorgeirsson, Snorri_S.
CS
     National Institute of Dental Research, National Institutes of Health,
     Bethesda, MD, 20892, USA
Proceedings of the National Academy of Sciences of the United States of
SO
     America (1995), 92(7), 2572-6
CODEN: PNASA6; ISSN: 0027-8424
PB
     National Academy of Sciences
DT
     Journal
     English
LA
     ANSWER 17 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
     1994:549708 CAPLUS
AN
     121:149708
```

PML/RAR.alpha.+ U937 mutant and NB4 cell lines: retinoic acid restores the

DN

TI

```
ΑU
      Testa, Ugo; Grignani, Francesco; Barberi, Tiziano; Fagioli, Marta;
      Masciulli, Rosalba; Ferrucci, Pier Francesco; Seripa, Davide; Camagna,
      Antonio; Alcalay, Myrian; et al.
      Department of Hematology and Oncology, Istituto Superiore di Sanita, Rome,
CS
SO
      Cancer Research (1994), 54(16), 4508-15
      CODEN: CNREA8; ISSN: 0008-5472
DT
      Journal
      English
LA
L4
      ANSWER 18 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
      1992:401809 CAPLUS
ΑN
      117:1809
DN
        ***Transforming***
                                ***growth***
                                                   ***factor*** -. ***beta***
TI
      (TGF-.beta.3) detection and inhibition, antibodies to TGF-.beta.3, and
      pharmaceutical compositions containing the pro region of TGF-.beta.3
IN
      Iwata, Kenneth K.; Foulkes, J. Gordon; Ten Dijke, Peter; Haley, John D.
      Oncogene Science, Inc., USA
PΑ
S<sub>0</sub>
      PCT Int. Appl., 98 pp.
      CODEN: PIXXD2
DT
      Patent
     English
LA
FAN.CNT 9
                        KIND DATE
     PATENT NO.
                                               APPLICATION NO. DATE
PΙ
     wo 9200330
                       A1
                               19920109
                                               wo 1991-US4540
                                                                   19910625
          W: AU, CA, JP
          RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE
     US 5262319
                               19931116
                                                US 1990-543341
                                                                   19900625
                        Α
     AU 9181838
                         Α1
                               19920123
                                                AU 1991-81838
                                                                   19910625
     AU 657913
                               19950330
                         В2
     EP 536275
                                                EP 1991-912638
                          Α1
                               19930414
                                                                   19910625
     EP 536275
                         в1
                               19980422
          R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE
05509312 T2 19931222 JP 1991-513051 19910625
     JP 05509312
     AT 165395
                               19980515
                                                AT 1991-912638
                                                                   19910625
     ES 2120416
                         Т3
                               19981101
                                                ES 1991-912638
                                                                   19910625
PRAI US 1990-543341
                               19900625
     US 1985-725003
                         В2
                               19850419
     US 1986-847931
                         В2
                               19860407
     US 1986-922121
                          В2
                               19861020
     US 1987-111022
                          A2
                               19871020
     US 1988-183824
                          В2
                               19880420
     US 1989-353410
                          В2
                               19890517
     WO 1991-US4540
                               19910625
                          Α
     ANSWER 19 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
L4
     1992:38680 CAPLUS
AN
DN
     116:38680
TI
     Desmin is present in proliferating rat muscle satellite cells but not in
     boyine muscle satellite cells
     Allen, Ronald E.; Rankin, Lucinda L.; Greene, Elizabeth A.; Boxhorn, Linda K.; Johnson, Sally E.; Taylor, Richard G.; Pierce, Paul R. Dep. Anim. Sci., Univ. Arizona, Tucson, AZ, 85721, USA Journal of Cellular Physiology (1991), 149(3), 525-35
ΑU
CS
S<sub>0</sub>
     CODEN: JCLLAX; ISSN: 0021-9541
DT
     Journal
LA
     English
L4
     ANSWER 20 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
AN
     1991:672656 CAPLUS
DN
     115:272656
                     ***transforming***
TI
     Recombinant
                                             ***arowth***
                                                                  ***factor***
        ***beta*** . analogs
     Cohen, Charles M.
IN
PA
     Creative Biomolecules, Inc., USA
SO
     PCT Int. Appl., 43 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
FAN, CNT 1
                                               APPLICATION NO. DATE
                   KIND DATE
     PATENT NO.
```

wo 1990-us6006

19901018

PΙ

wo 9105565

Al

19910502

```
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE 070393 AA 19910419 CA 1990-2070393 19901018
     CA 2070393
                                           AU 1991-68707
     AU 9168707
                                                            19901018
                       A1
                            19910516
     EP 496833
                                           EP 1990-917700
                                                           19901018
                            19920805
                       Α1
            AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE
     JP 05501500
                      T2
                            19930325
                                           JP 1991-500412
                                                            19901018
PRAI US 1989-422962
                            19891018
    wo 1990-us6006
                            19901018
    ANSWER 21 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN 1991:575892 CAPLUS
L4
ΑN
     115:175892
DN
     Inhibiting and stimulating effects of TGF-.beta.1 on osteoclastic bone
TI
     resorption in fetal mouse bone organ cultures
     Dieudonne, S. C.; Foo, P.; Van Zoelen, E. J. J.; Burger, E. H.
ΑU
     Acad. Cent. Dent., Vrije Univ., Amsterdam, 1081 BT, Neth.
CS
     Journal of Bone and Mineral Research (1991), 6(5), 479-87
SO
     CODEN: JBMREJ; ISSN: 0884-0431
DT
     Journal
LA
     English
L4
     ANSWER 22 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1991:528526 CAPLUS
ΑN
DN
     115:128526
     Tissue-derived tumor growth inhibitors, methods of preparation, and uses
TI
IN
     Iwata, Kenneth K.; Stephenson, John R.; Ten Dijke, Peter; Franco, Robert;
     Gold, Leslie I.; Foulkes, J. Gordon
PΑ
     Oncogene Science, Inc., USA
S0
     PCT Int. Appl., 190 pp.
     CODEN: PIXXD2
DT
     Patent
     English
LA
FAN.CNT 9
     PATENT NO.
                    KIND DATE
                                           APPLICATION NO. DATE
PΙ
     wo 9014360
                      Α1
                            19901129
                                           wo 1990-us2753
                                                           19900517
        W: AU, CA, JP
        RW: AT, BE, CH, DE, DK, ES, FR, GB, IT, LU, NL, SE
2056981 AA 19901118 CA 1990-2056981 19900517
     CA 2056981
     AU 9057293
                            19901218
                      A1
                                           AU 1990-57293
                                                            19900517
     AU 668072
                       В2
                            19960426
     JP 04505325
                                           JP 1990-508246
                      T2
                            19920917
                                                            19900517
     EP 508983
                                           EP 1990-908325
                      Α1
                            19921021
                                                            19900517
            AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE
                            19890517
PRAI US 1989-353410
                     Α
     wo 1990-us2753
                            19900517
L4
     ANSWER 23 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
ΑN
     1991:486162 CAPLUS
DN
     115:86162
    TI
ΑU
CS
50
     CODEN: MCEBD4; ISSN: 0270-7306
DT
     Journal
LA
     English
L4
     ANSWER 24 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1991:1783 CAPLUS
ΑN
DN
     114:1783
TI
     Cloning and expression of
                                 ***transforming***
                                                        ***growth***
       Purchio, Anthony F.; Madisen, Linda; Webb, Nancy
IN
PA
     Oncogen, L. P., USA
     Eur. Pat. Appl., 58 pp.
50
     CODEN: EPXXDW
DT
     Patent
LA
    English
FAN.CNT 2
     PATENT NO.
                      KIND DATE
                                           APPLICATION NO.
```

PΙ

EP 376785

Α2

19900704

19891214

EP 1989-403480

```
AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE
620 A 19930622 US 1989-446020 198
     US 5221620
                                                                 19891205
                              19900616
      CA 2005459
                                               CA 1989-2005459
                                                                 19891213
                         AA
      NO 8905029
                               19900618
                                               NO 1989-5029
                                                                 19891214
                         Α
     EP 676474
                         A1
                              19951011
                                               EP 1995-104223
                                                                 19891214
              AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE
     DK 8906383
                                              ĎK 1989-6383
                                                                 19891215
                              19900617
                         Α
                               19900621
     AU 8946835
                         Α1
                                               AU 1989-46835
                                                                 19891215
     AU 640115
                         В2
                              19930819
     ZA 8909623
                                               ZA 1989-9623
                               19900926
                                                                 19891215
                         Α
     CN 1045992
                               19901010
                                               CN 1989-109814
                                                                 19891216
     JP 05056783
                                               JP 1989-327054
                         Α2
                              19930309
                                                                 19891216
                              19881216
PRAI US 1988-285140
                         Α
                              19891205
     US 1989-446020
     US 1987-106752
                         B2
                              19871006
     US 1988-148267
                         В2
                              19880125
     US 1988-234065
                         В2
                              19880818
     EP 1989-403480
                         A3
                              19891214
L4
     ANSWER 25 OF 27
                       CAPLUS COPYRIGHT 2003 ACS on STN
     1990:31707 CAPLUS
ΑN
     112:31707
DN
     Cloning and expression of the gene for transforming growth factor B-2 in
TI
     mammalian cells
     Purchio, Anthony F.; Madisen, Linda; Webb, Nancy
IN
PA
     Oncogen, USA
     Fr. Demande, 59 pp.
SO
     CODEN: FRXXBL
DT
     Patent
LA
     French
FAN.CNT 2
     PATENT NO.
                        KIND
                              DATE
                                               APPLICATION NO.
                                                                 DATE
                              19890407
PΙ
     FR 2621324
                         Α1
                                               FR 1988-13046
                                                                 19881005
     FR 2621324
                         в1
                              19940218
     ZA 8807007
                              19900725
                         Α
                                              ZA 1988-7007
                                                                 19880920
     IL 103749
                         Α1
                              19941229
                                               IL 1988-103749
                                                                 19880929
     FI 8804546
                         Α
                              19890407
                                               FI 1988-4546
                                                                 19881003
     DK 8805563
                         Α
                              19890407
                                               DK 1988-5563
                                                                 19881005
     NO 8804429
                         Α
                                              NO 1988-4429
                              19890407
                                                                 19881005
     SE 8803528
                         Α
                              19890407
                                               SE 1988-3528
                                                                 19881005
                                               NL 1988-2442
     NL 8802442
                         Α
                               19890501
                                                                 19881005
     DE 3833897
                         Α1
                              19890503
                                               DE 1988-3833897
                                                                 19881005
     DE 3833897
                              19970320
                         C2
     CN 1035845
                              19890927
                         Α
                                               CN 1988-109075
                                                                 19881005
     ES 2012556
                         Α6
                              19900401
                                              ES 1988-3023
                                                                 19881005
     BE 1002693
                         Α5
                              19910507
                                              BE 1988-1141
                                                                 19881005
     CH 680002
                         Α
                              19920529
                                               CH 1988-3702
                                                                 19881005
     AT 8802454
                         Α
                              19940415
                                              AT 1988-2454
                                                                 19881005
     KR 9701236
                         В1
                              19970204
                                               KR 1988-12986
                                                                 19881005
     AU 8823451
                         A1
                              19890406
                                              AU 1988-23451
                                                                 19881006
     AU 630075
                         B2
                              19921022
                                              GB 1988-23448
     GB 2210620
                         A1
                              19890614
                                                                 19881006
     GB 2210620
                         B2
                              19920708
     JP 02000444
                                               JP 1988-251011
                         A2
                              19900105
                                                                 19881006
     AT 9201864
                                              AT 1992-1864
                         Α
                              19960515
                                                                 19920918
     AT 401938
                         В
                              19961227
     AT 9201865
                         Α
                              19960515
                                              AT 1992-1865
                                                                 19920918
     AT 401939
                         В
                              19961227
PRAI US 1987-106752
                         Α
                              19871006
     US 1988-148267
                         Α
                              19880125
     US 1988-234065
                         Α
                              19880818
     IL 1988-87877
                         A3
                              19880929
     AT 1988-2454
                              19881005
                         Α
L4
     ANSWER 26 OF 27 CAPLUS COPYRIGHT 2003 ACS on STN
     1989:109071 CAPLUS
AN
DN
     110:109071
     Regulation of skeletal muscle satellite cell proliferation and differentiation by ***transforming*** ***growth***
TI
                                                                       ***factor***
                     , insulin-like growth factor I, and fibroblast growth
     Allen, Ronald E.; Boxhorn, Linda K.
ΑU
```

CS Dep. Anim. Sci., Univ. Arizona, Tucson, AZ, 85721, USA SO Journal of Cellular Physiology (1989), 138(2), 311-15

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 4668.52 Seconds

(without alignments)

10489.161 Million cell updates/sec

Title: US-10-017-372E-8

Perfect score: 1197

Sequence: 1 atggcgccttcggggctgcg.....gttcctgcaagtgcagctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb pr:*

10: gb_ro:*

11: gb sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em hum:*

18: em_in:*

19: em mu:*

20: em om:*

21: em or:*

22: em ov:*

23: em_pat:*

24: em ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

```
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em htg vrt:*
38:
    em_sy:*
39:
    em htgo_hum: *
40:
    em_htgo_mus:*
    em_htgo_other:*
41:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		F				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
						7V220212 Common
1	1135.8				AX338213	AX338213 Sequence
2	1131	94.5	2221	4	AF461808	AF461808 Sus scrof
3	1131	94.5	3206	4	PIGTGFB1A	M23703 Sus scrofa
4	1129.4	94.4	1605	4	SSTGFBR	Y00111 Porcine mRN
5	1111.6	92.9	1750	4	GGTGFB1	X12373 Porcine mRN
6	999.8	83.5	1173	4	OATGFB1	X76916 O.aries mRN
7	967.8	80.9	1369	4	DOGTGFB1A	L34956 Canine tran
8	956.6	79.9	1561	9	AGMTGFB	M16658 Simian tran
9	956.6	79.9	1746	9	BC022242	BC022242 Homo sapi
10	956.6	79.9	1780	9	BC000125	BC000125 Homo sapi
11	956.6	79.9	1780	9	BC001180	BC001180 Homo sapi
12	956.6	79.9	1821	6	E03028	E03028 DNA encodin
13	956.6	79.9	2537	6	A06669	A06669 Synthetic m
14	955	79.8	2527	6	E00973	E00973 cDNA encodi
15	954.6	79.7	1173	9	BT007245	BT007245 Homo sapi
16	954.6	79.7	1173	12	BT007866	BT007866 Synthetic
17	952.4	79.6	1560	6	I06216	106216 Sequence 2
18	952.4	79.6	1560	6	I08268	108268 Sequence 2
19	945.4	79.0	1173	4	ECRGFB1	X99438 E.caballus
20	945.2	79.0	1176	6	AX615127	AX615127 Sequence
21	943.6	78.8	1176	6	AX481432	AX481432 Sequence
22	943.6	78.8	1176	6	AX615128	AX615128 Sequence
23	943.6	78.8	2745	9	HSTGFB1	X02812 Human mRNA
24	939	78.4	1187	4	AF175709	AF175709 Equus cab
25	936.2	78.2	1569	6	106221	106221 Sequence 3
26	927.8	77.5	1561	6	I08275	108275 Sequence 3
27	891	74.4	1597	10	AF191297	AF191297 Cavia por
28	854.2	71.4		10	RNTGFB1	X52498 Rat mRNA fo
29	847.8	70.8	1579	10	MUSTGFRNA	M13177 Mouse trans
30	847.8	70.8	1641	10	BC013738	BC013738 Mus muscu
31	847.8	70.8		10	MMU009862	AJ009862 Mus muscu
32	805.6	67.3		4	BOVTGFB	M36271 Bovine tran
33	804.6	67.2		10	AF480858	AF480858 Sigmodon

```
34
          682
               57.0
                       1675 6 I03310
                                                         103310 Sequence 1
    35
          654 54.6 1376 6 AX528533
                                                         AX528533 Sequence
        652.4 54.5 1389 6 AX528619
                                                         AX528619 Sequence
    36
   37
        591.4 49.4 1352 6 AX528535
                                                         AX528535 Sequence
   38
        586.6 49.0 1350 6 AX528615
                                                         AX528615 Sequence
        570.6
                       699 6 105434
                                                         105434 Sequence 4
   39
               47.7
                       489 6 AX455100
    40
         344
              28.7
                                                        AX455100 Sequence
                       469 10 MATGFB1
    41
        340.4
               28.4
                                                         X60296 M.auratus m
    42
        329.2 27.5 1256 5 CHKTGFB4
                                                         M31160 Gallus gall
    43
        310.2 25.9 339 6 AR036686
                                                         AR036686 Sequence
    44
        309.6 25.9 374 4 AF349538
                                                         AF349538 Canis fam
    45
       308.6 25.8 339 4 OCAF000133
                                                         AF000133 Oryctolag
                                   ALIGNMENTS
RESULT 1
AX338213
LOCUS
                                  1326 bp
                                             DNA
                                                     linear PAT 09-JAN-2002
           AX338213
DEFINITION Sequence 1 from Patent W00181404.
ACCESSION
           AX338213
           AX338213.1 GI:18128750
VERSION
KEYWORDS
SOURCE
           Sus scrofa (pig)
  ORGANISM Sus scrofa
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
           Strober, W., Nakamura, K., Kitani, A. and Fuss, I.J.
  AUTHORS
  TITLE
            Inducible plasmid vector encoding tgf-_g(b) and uses thereof
  JOURNAL
            Patent: WO 0181404-A 1 01-NOV-2001;
           THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
                    Location/Oualifiers
                    1. .1326
     source
                    /organism="Sus scrofa"
                    /mol_type="genomic DNA"
                    /db xref="taxon:9823"
     CDS
                    16. .1188
                    /note="unnamed protein product"
                    /codon start=1
                    /protein_id="CAD20538.1"
                    /db_xref="GI:18128751"
                    /translation="MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                    RIEAIRGOILSKLRLASPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                    YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                    KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                    LSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
                    RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD'I'
                    QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT
               263 a
                        438 c
                                 392 g
                                         233 t
ORIGIN
                         94.9%; Score 1135.8; DB 6; Length 1326;
  Query Match
  Best Local Similarity 97.8%; Pred. No. 6.3e-197;
```

2; Indels

1;

Matches 1171; Conservative 0; Mismatches

Qy	1	ATGGCGCCTTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT	60
Db	16	ATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCT	75
Qy	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	76	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	135
Qy	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	136	GTGAAGCGGAAGCCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTCGCC	195
Qу	181	AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	196	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGTACTGGCTCTT	255
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	256	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	315
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	316	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	375
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	376	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	435
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	436	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	495
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	496	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	555
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	556	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	615
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	616	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	675
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	676	GCCCACTCTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	735
Qy	721	TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	736	TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	795
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	796	ATGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGA	849
Qy	841	${\tt AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC}$	900

```
-----GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 891
Db
        901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
            892 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 951
Db
Qу
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
            952 GAACCCAAGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1011
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
            1012 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1071
Db
       1081 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
            Db
       1072 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1131
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
            1132 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1188
Db
RESULT 2
AF461808
LOCUS
          AF461808
                              2221 bp
                                       mRNA
                                             linear MAM 03-JAN-2002
DEFINITION Sus scrofa transforming growth factor beta 1 (TGFB1) mRNA, complete
          cds.
ACCESSION
          AF461808
VERSION
          AF461808.1 GI:18042250
KEYWORDS
          Sus scrofa (pig)
SOURCE
 ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
          1 (bases 1 to 2221)
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
 AUTHORS
          Polymorphism in the porcine transforming growth factor beta 1 gene
 TITLE
          Unpublished
 JOURNAL
REFERENCE
            (bases 1 to 2221)
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
 AUTHORS
          Direct Submission
 TITLE
          Submitted (20-DEC-2001) Institute of Animal Breeding Science,
 JOURNAL
          University of Bonn, Endenicher Allee 15, Bonn 53115, Germany
FEATURES
                 Location/Qualifiers
                 1. .2221
    source
                 /organism="Sus scrofa"
                 /mol type="mRNA"
                  /db_xref="taxon:9823"
                  /chromosome="6"
    gene
                 1. .2221
                 /gene="TGFB1"
    CDS
                 1. .1173
                 /gene="TGFB1"
                 /note="cytokine"
                 /codon_start=1
```

```
/product="transforming growth factor beta 1"
               /protein_id="AAL57902.1"
               /db xref="GI:18042251"
               translation="MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK/
               RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
               YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
               KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
               LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRH
               RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
               QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
   3'UTR
               1174. .2221
               /qene="TGFB1"
BASE COUNT
           504 a
                  616 C
                         649 g
                               452 t.
ORIGIN
 Query Match
                   94.5%;
                        Score 1131; DB 4; Length 2221;
 Best Local Similarity
                  97.6%;
                        Pred. No. 4.4e-196;
 Matches 1168; Conservative
                        0; Mismatches
                                        Indels
                                               24;
                                                  Gaps
        Qу
          Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTCGCC 180
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGTACTGGCTCTT 240
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
          Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
          421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Db
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
          Db
       481 AAGTTAAAAGTGGAGCACCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qу
```

Db	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
Db	601	
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720
Db	661	GCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Db	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Db	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGA 834
Qу	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Db	835	GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 876
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Db	877	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 936
Qу	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Db	937	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 996
Qy 1	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Db	997	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1056
Qy 1	1081	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Db 1	L057	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1116
Qy 1	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Db 1	1117	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1173
RESULT 3 PIGTGFB1A LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	N S M M t S N S E M 1 K	IGTGFB1A 3206 bp mRNA linear MAM 31-MAR-1995 us scrofa transforming growth factor beta-1 mRNA, complete cds. 23703 23703.1 GI:755044 ransforming growth factor-beta-1. us scrofa (pig) us scrofa ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (bases 1 to 3206) ondaiah, P., Van Obberghen-Schilling, E., Ludwig, R.L., Dhar, R., porn, M.B. and Roberts, A.B.

```
TITLE
          cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
          Evidence for alternate splicing and polyadenylation
 JOURNAL
          J. Biol. Chem. 263 (34), 18313-18317 (1988)
          89054010
 MEDLINE
  PUBMED
          2461367
COMMENT
          On Apr 1, 1995 this sequence version replaced gi:341017.
          Original source text: Sus scrofa (strain miniature swine) cDNA to
FEATURES
                 Location/Qualifiers
    source
                 1. .3206
                 /organism="Sus scrofa"
                 /mol type="mRNA"
                 /strain="miniature swine"
                 /db xref="taxon:9823"
                 /cell type="peripheral blood lymphocyte"
    gene
                 1. .3206
                 /gene="TGF-beta-1"
    CDS
                 906. .2078
                 /gene="TGF-beta-1"
                 /codon start=1
                 /product="transforming growth factor-beta-1"
                 /protein id="AAA64616.1"
                 /db xref="GI:755045"
                 /translation="MPPSGLRLLPLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                 RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                 YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                 KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                 {\tt LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH}
                 RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                 QYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS"
                 3186. .3191
    polyA_signal
                 /gene="TGF-beta-1"
    polyA site
                 3206
                 /gene="TGF-beta-1"
BASE COUNT
             645 a
                   1041 c
                            924 q
                                    596 t
ORIGIN
 Query Match
                      94.5%; Score 1131; DB 4; Length 3206;
 Best Local Similarity
                     97.6%; Pred. No. 4.3e-196;
 Matches 1168; Conservative
                           0; Mismatches
                                          5;
                                             Indels
                                                     24; Gaps
                                                                1:
          Qу
            Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qy
            Db
        966 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 1025
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
            Db
       1026 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTCGCC 1085
        181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
            1086 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGTACTGGCTCTT 1145
Db
```

Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1146	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	1205
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1206	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	1265
QУ	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1266		1325
QУ	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1326	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	1385
QУ	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1386	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	1445
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1446	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	1505
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1506	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	1565
Qу		GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db		GCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db		TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	
Qу		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCGAGACTAC	
Db		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCGCCGA	
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db			
Qу		TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	
Db		TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	
Qy		GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	
Db	1842	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1901
Qy		GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	
Db	1902	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1961
Qу	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140

```
1962 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 2021
Db
Qу
        1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
             2022 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 2078
Db
RESULT 4
SSTGFBR
LOCUS
                                  1605 bp
           SSTGFBR
                                            mRNA
                                                    linear
                                                            MAM 27-MAR-1995
DEFINITION
          Porcine mRNA for transforming growth factor-beta (TFG) precursor.
ACCESSION
           Y00111
VERSION
           Y00111.1 GI:2129
KEYWORDS
           transforming growth factor-beta.
SOURCE
           Sus scrofa (pig)
 ORGANISM Sus scrofa
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
              (bases 1 to 1605)
           Derynck, R. and Rhee, L.
 AUTHORS
 TITLE
           Sequence of the porcine transforming growth factor-beta precursor
           Nucleic Acids Res. 15 (7), 3187 (1987)
 JOURNAL
 MEDLINE
           87174844
  PUBMED
           3470708
FEATURES
                    Location/Qualifiers
                    1. .1605
    source
                    /organism="Sus scrofa"
                    /mol type="mRNA"
                    /db xref="taxon:9823"
                    /tissue type="ovary"
                    /clone lib="lambda qt10"
    CDS
                    404. .1576
                    /note="TFG-beta precursor (AA 1-390)"
                    /codon start≈1
                    /protein id="CAA68291.1"
                    /db xref="GI:2130"
                    /db_xref="SWISS-PROT:P07200"
                    /translation="MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                    RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                    YYAKEVTRVLMLESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                    KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                    LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
                    RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                    OYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS"
                    1238. .1573
    mat peptide
                    /product="mature TFG-beta"
                    647. .655
    misc feature
                    /note="pot. N-glycosylation site"
                    809. .817
    misc feature
                    /note="pot. N-glycosylation site"
BASE COUNT
               298 a
                       572 c
                               437 q
                                        298 t
ORIGIN
 Query Match
                        94.4%; Score 1129.4; DB 4; Length 1605;
 Best Local Similarity
                        97.5%; Pred. No. 9e-196;
 Matches 1167; Conservative 0; Mismatches
                                               6; Indels
                                                            24; Gaps
                                                                         1;
```

Qу	1	ATGGCGCCTTCGGGGCTGCTGCCGCTGCTGCTGCTGCTGCT	60
Db	404	ATGCCGCCTTCGGGGCTGCTGCCGCTGCTGCTGCTGCTGCT	463
Qу	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	464	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	523
Qy	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	524	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTCGCC	583
Qу	181	AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	584	AGCCCCCGAGCCAGGGGGACGTGCCGGCCCGCTGCCTGAGGCCGTACTGGCTCTT	643
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	644	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	703
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	704	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGCTGGAAAGCGGCAACCAAATC	763
Qу	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	764		823
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	824	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	883
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	884	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	943
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	944	TACCTCAGCAACCGGCTGCTCGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	1003
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1004	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	1063
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1064	GCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	1123
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1124	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	1183
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1184	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGA	1237

```
Qу
        841 AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
                           Db
       1238 -----GCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAC 1279
Oy
        901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
            1280 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 1339
Db
Qу
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
            1340 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1399
Db
Qу
        1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
            Dh
       1400 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1459
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
            1460 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1519
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
QУ
            1520 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1576
Db
RESULT 5
GGTGFB1
LOCUS
          GGTGFB1
                               1750 bp
                                        mRNA
                                               linear
                                                       MAM 27-MAR-1996
DEFINITION Porcine mRNA for transforming growth factor-beta 1.
ACCESSION
          X12373
          X12373.1 GI:63808
VERSION
KEYWORDS
          transforming growth factor-beta 1.
SOURCE
          Sus scrofa (pig)
 ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
             (bases 1 to 1750)
 AUTHORS
          Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
 TITLE
          Nucleotide sequence of chicken transforming growth factor-beta 1
          (TGF-beta 1)
 JOURNAL
          Nucleic Acids Res. 16 (17), 8730 (1988)
          88335639
 MEDLINE
  PUBMED
          3166520
REFERENCE
            (bases 1 to 1750)
 AUTHORS
          Jakowlew, S.B.
 TITLE
          Direct Submission
          Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
 JOURNAL
          health, National Cancer Institute, Laboratory of Chemoprevention,
          Building 41, Room B902, Bethesda, Maryland 20892, USA
COMMENT
          The submitters believe that the chicken cDNA library was
          contaminated with porcine cDNA, and that the sequence is infact
          porcine TGF-beta-1.
                             27-MAR-1996.
FEATURES
                  Location/Oualifiers
                  1. .1750
    source
                  /organism="Sus scrofa"
                  /mol type="mRNA"
                  /strain="white leghorn"
```

```
/db xref="taxon:9823"
                /clone="pTGFB-ChX119"
                /cell type="chondrocyte"
   gene
                1. .1750
                /gene≈"TGF-beta 1"
    5'UTR
                1. .446
                /gene="TGF-beta 1"
    CDS
                447. .1622
                /gene="TGF-beta 1"
                /codon start=1
                /product="transforming growth factor"
                /protein id="CAA30933.1"
                /db xref="GI:63809"
                /db xref="SWISS-PROT:P07200"
                /translation="MPPSGPGLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                KLKVEQHVELYQKYSNDSWGYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                \verb|LSAHCSCDSKDNTLHVEINAGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSR|
                HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD
                TQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                1285. .1619
   mat peptide
                /gene="TGF-beta 1"
                1620. .1750
   3'UTR
                /gene="TGF-beta 1"
BASE COUNT
            325 a
                   627 c
                          479 q
                                  319 t
ORIGIN
                    92.9%; Score 1111.6; DB 4; Length 1750;
 Query Match
 Best Local Similarity
                    97.0%; Pred. No. 1.6e-192;
 Matches 1164; Conservative
                          0; Mismatches
                                        9; Indels
                                                  27; Gaps
                                                             2:
         Qу
           Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           507 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 566
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           567 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTCGCC 626
Db
        181 AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           627 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGGTGCCTGAGGCCGTACTGGCTCTT 686
Db
        241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           Db
        687 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 746
        301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           747 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 806
Db
        361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
```

Db	807		866
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	867		926
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	927		986
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	987	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	1046
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1047		1106
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC	717
Db	1107	GCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGCAGGGTTC	1166
Qy	718	AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	777
Db	1167	AATTCTGGCCGCCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	1226
Qу	778	CTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	1227	CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGA	1283
Qу	838	TACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
Db	1284	GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	1322
Qу	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
Db	1323	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	1382
Qу	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1017
Db	1383	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1442
Qу	1018	CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG	1077
Db	1443	CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG	1502
Qy	1078	GCGGCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC	1137
Db	1503	GCGGCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC	1562
Qу	1138	CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA	1197
Db	1563	CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA	1622

```
OATGFB1
                                                         MAM 18-APR-1995
LOCUS
          OATGFB1
                                1173 bp
                                          mRNA
                                                 linear
DEFINITION O.aries mRNA for transforming growth factor-beta I.
ACCESSION
         X76916
          X76916.1 GI:496648
VERSION
KEYWORDS
          TGF-beta 1; transforming growth factor-beta 1.
          Ovis aries (sheep)
SOURCE
 ORGANISM
          Ovis aries
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
          Bovidae; Caprinae; Ovis.
REFERENCE
 AUTHORS
          Woodall, C.J., McLaren, L.J. and Watt, N.J.
 TITLE
          Sequence and chromosomal localisation of the gene encoding ovine
          latent transforming growth factor-beta 1
  JOURNAL
          Gene 150 (2), 371-373 (1994)
          95121932
 MEDLINE
          7821809
  PUBMED
REFERENCE
             (bases 1 to 1173)
 AUTHORS
          Woodall, C.
 TITLE
          Direct Submission
 JOURNAL
          Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of
          Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
          Edinburgh EH9 IQH, UK
FEATURES
                  Location/Qualifiers
                   1. .1173
    source
                   /organism="Ovis aries"
                   /mol type="mRNA"
                   /db xref="taxon:9940"
    CDS
                   1. .1173
                   /codon start=1
                   /product="transforming growth factor-beta 1"
                   /protein_id="CAA54242.1"
                   /db xref="GI:496649"
                   /db xref="SWISS-PROT:P50414"
                   /translation="MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRK
                  GI EA I RGQI LSKLRLASPPSQGDVPPGPLPEA I LALYNSTRDRVAGESAETEPEPEAD
                   YYAKEVTRVLMVEYGNKI YDKMKSSSHSI YMFFNTSELREAVPEPVLLSRADVRLLRL
                   KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREE1EGFR
                  LSAHCSCDSKDNTLOVDINGFSSGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRH
                  RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                  QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
    mat peptide
                   835. .1170
                   /product="transforming growth factor-beta 1"
BASE COUNT
              245 a
                      378 c
                              336 g
                                      214 t
ORIGIN
 Query Match
                       83.5%; Score 999.8; DB 4; Length 1173;
 Best Local Similarity
                       90.7%; Pred. No. 3.7e-172;
 Matches 1086; Conservative
                             0; Mismatches
                                            87;
                                                 Indels
                                                         24; Gaps
Qу
          Db
          Qу
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
```

Dp	61	CTGACGCCTGGCCGGCCGGTCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Qу	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	121	GTGAAGCGGAAGGCCATCCGCGGTCAGATTTTGTCCAAACTTCGGCTCGCC	180
Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	181	AGTCCCCGAGCCAGGGGACGTGCCACCCGGCCCGCTGCCCGAGGCCATACTGGCCCTT	240
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	241	TACAACAGTACCCGCGACCGGGTGGCCGGGGAAAGTGCCGAAACGGAGCCTGAGCCAGAG	300
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAATACGGCAACAAAATC	360
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	361	TATGACAAAATGAAGTCTAGCTCGCACAGCATATATATGTTCTTCAACACGTCCGAGCTC	420
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	421	CGGGAAGCAGTGCCTGAACCTGTGTTGCTCTCTCGGGCAGACGTGCGCCTGCTGAGGCTC	480
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	481	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATATAGCAACAATTCCTGGCGC	540
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	541	TACCTCAGCAACCGGCTGCTCGCCCCCAGCGACTCACCGGAGTGGCTGTCCTTTGACGTC	600
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	601	ACTGGAGTTGTGCGGCAGTGGCTGACCCACAGAGAGGAAATAGAAGGCTTTCGCCTCAGT	660
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	661	GCCCACTGTTCCTGTGACAGTAAGGATAACACGCTTCAAGTGGACATCAACGGGTTCAGT	720
Qу	721	TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	721	TCCGGCCGCGGGGTGACCTCGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCCGAGACTAC	840
Db	781	ATGGCCACCCCTCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGCCGA	834
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	835		876
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	877	TGCTGTCTCGTCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAC	936

```
961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
            Db
         937 GAACCCAAGGGCTACCACGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTG 996
        1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
            Db
         997 GACACACAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCATCGGCG 1056
        1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
            Db
        1057 GCGCCGTGCTGCCTCAGGCGCTGGAACCCCTGCCCATCGTGTACTACGTGGGCCGC 1116
        1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
             Db
        1117 AAGCCCAAGGTGGAGCAGTTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1173
RESULT 7
DOGTGFB1A
LOCUS
          DOGTGFB1A
                                1369 bp
                                          mRNA
                                                 linear
                                                         MAM 30-OCT-1994
DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete
          cds.
ACCESSION
          L34956
          L34956.1 GI:516071
VERSION
KEYWORDS
          homologue; transforming growth factor-beta 1.
SOURCE
          Canis familiaris (dog)
 ORGANISM Canis familiaris
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
             (bases 1 to 1369)
 AUTHORS
          Manning, A.M., Auchampach, J.A., Drong, R.F. and Slightom, J.L.
          Cloning of a canine cDNA homologous to human transforming growth
 TITLE
           factor-beta 1 (TGFbeta1)
 JOURNAL
          Unpublished (1994)
COMMENT
          Original source text: Canis familiaris adult jugular vein
           endothelial cDNA to mRNA.
FEATURES
                  Location/Qualifiers
                   1. .1369
    source
                   /organism="Canis familiaris"
                   /mol_type="mRNA"
                   /db_xref="taxon:9615"
                   /cell type="LPS-activated"
                   /tissue type="jugular vein endothelial"
                   /dev stage="adult"
                   1. .1369
    gene
                   /gene="TGFB1"
    5'UTR
                   1. .57
                   /gene="TGFB1"
    CDS
                   58. .1230
                   /gene="TGFB1"
                   /function="anti-inflammatory agent"
                   /note="precursor"
                   /codon start=1
                   /product="transforming growth factor-beta 1"
                   /protein id="AAA51458.1"
                   /db xref="GI:516072"
```

RIEAIRGQILSKLRLSSPPSQGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEAD YYAKEVTRVLMVENTNKI YEKVKKSPHSI YMLFNTSELREAVPEPVLLSRAELRLLRL KLKAEQHVELYQKYSNDSWRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFR LSAHCSCDSKDNTLOVDINGFSSSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRO RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS" mat_peptide 1039. .1227 /gene="TGFB1" /product="transforming growth factor-beta 1" 3'UTR 1231. .1369 /gene="TGFB1" BASE COUNT 264 a 473 c 415 g 216 t 1 others ORIGIN Query Match 80.9%; Score 967.8; DB 4; Length 1369; Best Local Similarity 89.1%; Pred. No. 2.4e-166; Matches 1066; Conservative 0; Mismatches 107; Indels 24; Gaps 1; Qу Db 61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120 Qу 118 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAACTG 177 Db Qу 121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180 178 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCTCC 237 Db Qу 181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240 Db 238 AGCCCCCGAGCCAGGGGAGGTGCCGCCCGTGCCCGAGGCCGTGCTGGCCCTC 297 241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300 Qу 298 TACAACAGCACCCGCGACCGGGTGGCGGGGGGGGGGGCCCGAGCCCGAGCCCGAG Db 301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360 Qу Db 358 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAACACCAACAAAATC 417 361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420 Qу 1111 111 1111 418 TATGAGAAAGTCAAGAAAAGTCCGCACAGCATATATATGCTCTTCAACACATCAGAGCTC 477 Db 421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480 Qу Db 478 CGAGAAGCAGTGCCTGAGCCCGTCTTGCTCTCCCGGGCAGAGTTGCGCCTGCTGAGGCTC 537 481 AAGTTAAAAGTGGAGCACCTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540 Qу 538 AAGTTAAAAGCGGAGCATGTGGAGCTGTACCAGAAATATAGCAATGATTCCTGGCGC 597 Db

541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600

Qу

/translation="MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRK

Db	598	TACCTCAGCAACCGGCTGCTGGCGCCCAGCGACACGCCAGAATGGCTGTCCTTTGATGTC	657
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	658	ACTGGAGTCGTGAGGCAGTGGCTGAGCCATGGAGGGGAAGTCGAGGGCTTTCGCCTCAGT	717
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	718	GCCCACTGTTCCTGTGACAGCAAAGATAACACACTGCAAGTAGACATTAACGGGTTCAGT	777
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	778	TCCAGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGACCCTTCCTGCTCCTC	837
Qу	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	838	ATGCCACCCCACTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCAGCGCCG	890
Qу	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	891		933
Qу	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
		TGCTGCGTCCGGCAGCTCTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCAT	
		GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	
		GAGCCCAAGGGTTACCACGCTAACTTCTGCCTGGGGCCCTGCCCCTACATTTGGAGCCTG	
		GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	
		GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	
		GCGCCGTGCTGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	
		GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	
		AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 119	
Db 1	.174	AAGCCCAAGGTGGAGCAGCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 123	30
RESULT 8 AGMTGFB LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	M S M M S C C C C C C C C C C C C C C C	GMTGFB 1561 bp mRNA linear PRI 27-APR- imian transforming growth factor-beta (TGF) mRNA, complete cds 16658 16658.1 GI:176552 rowth factor; transforming growth factor-beta. ercopithecus aethiops (African green monkey) ercopithecus aethiops	3.
REFERENCE AUTHORS	M: C: 1	ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston ammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; ercopithecinae; Cercopithecus. (bases 1 to 1561) harples,K., Plowman,G.D., Rose,T.M., Twardzik,D.R. and	n ⊥ ;

```
Purchio, A.F.
 TITLE
          Cloning and sequence analysis of simian transforming growth
          factor-beta cDNA
         DNA 6 (3), 239-244 (1987)
 JOURNAL
 MEDLINE
          87246074
  PUBMED
         3474130
COMMENT
          Original source text: African green monkey cells (cell line
          BSC-40), cDNA to mRNA, clone pTGF-beta-2.
FEATURES
                 Location/Qualifiers
                 1. .1561
    source
                 /organism="Cercopithecus aethiops"
                 /mol type="mRNA"
                 /db xref="taxon:9534"
    CDS
                 262. .1434
                 /note="transforming growth factor-beta precursor"
                 /codon start=1
                 /protein_id="AAA35369.1"
                 /db xref="GI:176553"
                 /translation="MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRK
                 RIETIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                 YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                 KLKVEQHVELYQKYSNNSWRYLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFR
                 LSAHCSCDSKDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                 RRALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                 QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
    sig peptide
                 262. .1095
                 /note="transforming growth factor-beta signal peptide"
    mat peptide
                 1096. .1431
                 /product="transforming growth factor-beta"
BASE COUNT
             301 a
                    547 c
                            446 q
                                   267 t
ORIGIN
 Query Match
                     79.9%; Score 956.6; DB 9; Length 1561;
 Best Local Similarity
                     88.5%; Pred. No. 2.6e-164;
 Matches 1059; Conservative
                           0; Mismatches 114; Indels
                                                    24; Gaps
          Qу
           Db
         61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           322 CTGACGCCTAGCCGGCCGCCGCAGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 381
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           382 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 441
Db
        181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
QУ
           442 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 501
Db
        241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           Db
        502 TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGAGTGCGGAGCCGGAGCCCGAACCGGAG 561
        301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
QУ
```

Db	562		621
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	622	TATGACAAGTTCAAGCAGAGCACACACACACATATATATGTTCTTCAACACATCAGAGCTC	681
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	682	CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	741
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	742	AAGTTAAAAGTGGAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	801
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	802	TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	861
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	862	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	921
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	922	GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	981
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	982		1041
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1042	ATGGCCACCCCACTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA	1095
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1096		1137
Qу	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1138	TGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1197
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1198	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG	1257
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1258	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG	1317
Qy	1081	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1318	GCGCCGTGCTGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1377
Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 119	97

```
RESULT 9
BC022242
                                                       linear
                                                                PRI 04-FEB-2002
LOCUS
            BC022242
                                    1746 bp
                                               mRNA
DEFINITION Homo sapiens, clone MGC:22008 IMAGE:4399762, mRNA, complete cds.
ACCESSION
           BC022242
VERSION
            BC022242.1 GI:18490115
KEYWORDS
           MGC.
SOURCE
           Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            1
               (bases 1 to 1746)
  AUTHORS
            Strausberg, R.
            Direct Submission
  TITLE
            Submitted (01-FEB-2002) National Institutes of Health, Mammalian
  JOURNAL
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
  REMARK
COMMENT
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site:
                            http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 27 Row: e Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES
                     Location/Qualifiers
                     1. .1746
     source
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="MGC:22008 IMAGE:4399762"
                     /tissue type="Duodenum, adenocarcinoma"
                     /clone lib="NIH MGC 88"
                     /lab host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS
                     370. .1542
                     /codon start≈1
                     /product="Unknown (protein for MGC:22008)"
                     /protein id="AAH22242.1"
                     /db xref="GI:18490116"
                     /translation="MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
```

RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD

YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"

BASE COUNT 376 a 612 c 472 g 286 t ORIGIN

Best		79.9 imilarity 88.5 ; Conservative	%; Pred.		e-164;	Length Indels		Gaps	1;
Qу	1	ATGGCGCCTTCGGGGC							60
Db	370	 ATGCCGCCCTCCGGGC							429
Qу	61	CTGACGCCTGGCCGGC							120
Db	430	CTGACGCCTGGCCGGC							489
Qу	121	GTGAAGCGGAAGCGCA							180
Db	490	GTGAAGCGGAAGCGCA							549
Qy	181	AGCCCCCGAGCCAGG							240
Db	550	AGCCCCCGAGCCAGG							609
Qy	241	TACAACAGTACCCGCG							300
Db	610	TACAACAGCACCCGCG							669
Qу	301	GCGGACTACTACGCCA						CAAATC	360
Db	670	ĠĊĊĠŔĊŦŔĊŦŔĊĠĊĊŔ							729
Qу	361	TATGATAAATTCAAGG							420
Db	730	TATGACAAGTTCAAGC							789
Qy	421	CGGGAAGCGGTGCCGG		TTGCTCTCT(480
Db	790	CGAGAAGCGGTACCTG		rigererec	CGGGCAG2	ÄĠĊŦĠĊĠī	CTGCTG	AGGCTC	849
Qу	481	AAGTTAAAAGTGGAGC							540
Db	850	AAGTTAAAAGTGGAGC						TGGCGA	909
Qу	541	TACCTCAGCAACCGGC		CCAGTGAC		AGTGGCTG	TCCTTT	GATGTC	600
Db	910	TACCTCAGCAACCGGC	rgctggcad	CCAGCGAC	rcgccag <i>i</i>	AGTGGTTA	TĊŦŦŦŦ	GATGTC	969
Qy	601	ACCGGAGTTGTGCGGC							660
Db	970	ACCGGAGTTGTGCGGC							1029
Qy	661	GCCCACTCTTCCTCTG	ACAGCAAAC	GATAACACA	CTCCACG:	rggaaati	AACGGG	TTCAAT	720

Db	103	
Qy	72	1 TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Db	109	
Qy	78	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Db	115	D ATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA 1203
Qy	84	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Db	120	4GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1245
Qy	90	1 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Db	124	5 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1305
Qy	96	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Db	130	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1365
Qу	102	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Db	136	6 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1425
Qy	108	1 GCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Db	142	6 GCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1485
QУ	114	1 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Db	148	6 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1542
RESULT 1 BC000125 LOCUS DEFINITI	ON	BC000125 1780 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, Similar to transforming growth factor, beta 1, clone
ACCESSIO	N	MGC:3119 IMAGE:3351664, mRNA, complete cds. BC000125 BC000125.1 GI:12652748
VERSION KEYWORDS SOURCE		MGC. Homo sapiens (human)
ORGANI	SM	Homo sapiens (Human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHOR TITLE	S	Strausberg,R. Direct Submission
JOURNA	L	Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
		Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK COMMENT		NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk

```
cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Genome Sequence Centre,
          BC Cancer Agency, Vancouver, BC, Canada
          info@bcqsc.bc.ca
          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
          Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
          Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
          Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
          Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
          Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
          Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
          George Yang, Scott Zuyderduyn, Marco Marra.
          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 6 Row: e Column: 11
          This clone was selected for full length sequencing because it
          passed the following selection criteria: Hexamer frequency ORF
          analysis.
FEATURES
                  Location/Qualifiers
                  1. .1780
    source
                  /organism="Homo sapiens"
                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="MGC:3119 IMAGE:3351664"
                  /tissue type="Eye, retinoblastoma"
                  /clone_lib="NIH_MGC_16"
                  /lab host="DH10B-R"
                  /note="Vector: pOTB7"
    CDS
                  447. .1619
                  /codon start=1
                  /product="Similar to transforming growth factor, beta 1"
                  /protein id="AAH00125.1"
                  /db xref="GI:12652749"
                  /translation="MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                  RIEAIRGOILSKLRLASPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                  YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR
                  LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                  RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                  QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT
              341 a
                      648 c
                              493 q
                                      298 t
ORIGIN
 Query Match
                       79.9%; Score 956.6; DB 9; Length 1780;
                       88.5%; Pred. No. 2.6e-164;
 Best Local Similarity
 Matches 1059; Conservative
                             0; Mismatches 114; Indels
          61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
```

Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

Qу

Db

Qу

Db	507	CTGACGCCTGGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	566
Qу	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	567	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	626
Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	627	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGCCC	686
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	687	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	746
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	747	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	806
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	807	TATGACAAGTTCAAGCAGAGTACACACACACACATCAGAGCTC	866
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	867	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	926
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	927	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	986
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	987	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1046
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1047	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1106
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1107	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1166
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1167	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1226
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1227	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGGCACCGCCGA	1280
QY	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1281		1322
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1323	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1382

Qу	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Db	1383	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1442
Qу	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Db	1443	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1502
Qу	1081	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Db	1503	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1562
Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Db	1563	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1619

RESULT 11 BC001180

LOCUS BC001180 1780 bp mRNA linear PRI 12-JUL-2001 DEFINITION Homo sapiens, Similar to transforming growth factor, beta 1, clone MGC:2323 IMAGE:3356605, mRNA, complete cds.

ACCESSION BC001180

VERSION BC001180.1 GI:12654682

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1780)

AUTHORS Strausberg, R.
TITLE Direct Submission

JOURNAL Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

```
Series: IRAL Plate: 6 Row: e Column: 10
         This clone was selected for full length sequencing because it
         passed the following selection criteria: matched mRNA gi: 37097.
FEATURES
                Location/Oualifiers
                1. .1780
   source
                /organism="Homo sapiens"
                /mol type="mRNA"
                /db xref="taxon:9606"
                /clone="MGC:2323 IMAGE:3356605"
                /tissue type="Eye, retinoblastoma"
                /clone lib="NIH MGC 16"
                /lab host="DH10B-R"
                /note="Vector: pOTB7"
   CDS
                447. .1619
                /codon start=1
                /product="Similar to transforming growth factor, beta 1"
                /protein_id="AAH01180.1"
                /db xref="GI:12654683"
                /translation="MPPSGLRLLLLLLLLLLVLTPGRPAAGLSTCKTIDMELVKRK
                RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR
                LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                OYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS"
                                 298 t
BASE COUNT
            341 a
                   648 c
                          493 q
ORIGIN
 Query Match
                    79.9%; Score 956.6; DB 9; Length 1780;
                   88.5%; Pred. No. 2.6e-164;
 Best Local Similarity
                        0; Mismatches 114; Indels
 Matches 1059; Conservative
                                                 24; Gaps
                                                           1;
Qу
         Db
       61 CTGACGCCTGGCCGGCCGCCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           507 CTGACGCCTGGCCGGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 566
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           567 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 626
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAUTUTUGAACCGGAGCCCGAGCCAGAG 300
Qу
           687 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGATGCAGAACCGGAGCCCGAGCCTGAG 746
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           747 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 806
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
QУ
```

Db	807	TATGACAAGTTCAAGCAGAGTACACACACACATATATATGTTCTTCAACACATCAGAGCTC	866
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	867	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	926
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	927		986
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	987	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1046
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1047	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1106
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1107	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1166
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1167	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1226
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCGCGAGACTAC	840
Db	1227	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1280
Qу	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1281	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC	1322
Qy	901	TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1323	TGCTGCGTGCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1382
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1383	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1442
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1443	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG	1502
Qу	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1503		1562
Qу	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 119	97
Db	1563	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 16:	19

```
E03028
LOCUS
           E03028
                                             RNA
                                                    linear PAT 29-SEP-1997
                                  1821 bp
DEFINITION DNA encoding human prepro TGF-betal.
ACCESSION
           E03028
VERSION
           E03028.1 GI:2171250
KEYWORDS
           JP 1991180192-A/1.
SOURCE
           Homo sapiens (human)
 ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              (bases 1 to 1821)
REFERENCE
 AUTHORS
           Ohashi, H., Ishii, Y., Miyata, Y., Miyazono, K., Miyagawa, K. and
           Takaku, F.
 TITLE
           PRODUCTION OF HUMAN PRO-TGF-BETA1 BY GENETIC RECOMBINATION
 JOURNAL
           Patent: JP 1991180192-A 1 06-AUG-1991;
           KIRIN BREWERY CO LTD
COMMENT
           OS
                Homo sapiens (human)
           PN
                JP 1991180192-A/1
           PD
                06-AUG-1991
           PF
                07-DEC-1989 JP 1989318243
                OHASHI HIDEYA, ISHII YASUYUKI, MIYATA YOSHINORI, PI
                                                                    MIYAZONO
           KOHEI.
                MIYAGAWA KIYOSHI, TAKAKU FUMIMARO
           ΡI
           PC
                C12P21/00, C07K13/00, C12N5/10, C12N15/18//C12Q1/68, (C12P21/00,
           РC
                C12R1:91),
           PC
                (C12N15/18, C12R1:91);
                strandedness: Double;
           CC
           CC
                topology: Linear;
           CC
                hypothetical: No;
           CC
                anti-sense: No;
           CC
                *source: tissue type=placenta;
           CC
                *source: clone=pVC19-TGF;
           FΗ
                Key
                               Location/Qualifiers
           FΗ
           FT
                5'UTR
                               1. .510
           FT
                               511. .1683
                CDS
                               /product='human prepro TGF-betal' FT
           FT
           sig_peptide
                           511. .597
                               598. .1680
           FT
                mat_peptide
                               /note='human pro TGF-betal'
           FT
           FT
                mat_peptide
                               1345. .1680
           FT
                               /product='human TGF-beta1'
           FT
                3'UTR
                               1684. .1820.
FEATURES
                    Location/Qualifiers
    source
                    1. .1821
                    /organism="Homo sapiens"
                    /mol type="genomic RNA"
                    /db xref="taxon:9606"
BASE COUNT
               326 a
                        679 c
                                508 g
                                         308 t
ORIGIN
 Query Match
                         79.9%;
                                Score 956.6; DB 6; Length 1821;
 Best Local Similarity
                        88.5%; Pred. No. 2.6e-164;
 Matches 1059; Conservative
                               0; Mismatches 114;
                                                    Indels
                                                             24; Gaps
           Qу
```

Db	512	ATGCCGCCCTCCGGGCTGCTGCTGCCGCTGCTGCTGCTGCT	571
Qy	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	572	CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	631
Qy	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	632	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	691
Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	692	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	751
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	752	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	811
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	812	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	871
Qy	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	872	TATGACAAGTTCAAGCAGAGTACACACACACACATCAGAGCTC	931
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	932	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGAGGCTC	991
Qу		AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	
Db		AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	
Qу		TACCTCAGCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	
Db		TACCTCAGCAACCGGCTGCTGGCACCCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	
Qу		ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	
Db		ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	
Qy		GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	
Db		GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	
Qy		TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	
Db		ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	
Qу		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	
Db		ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	
Qy		AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	
Db	1346		1387

```
Qу
        901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
            Db
       1388 TGCTGCGTGCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1447
        961 GAACCCAAGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
            Db
       1448 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1507
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
QУ
            Db
       1508 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1567
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
            1568 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1627
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
QУ
            1628 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1684
Db
RESULT 13
A06669
LOCUS
          A06669
                               2537 bp
                                        mRNA
                                               linear
                                                       PAT 29-JUL-1993
DEFINITION
          Synthetic mRNA for preTGF-Betal.
ACCESSION
          A06669
          A06669.1 GI:412940
VERSION
KEYWORDS
SOURCE
          synthetic construct
 ORGANISM
          synthetic construct
          artificial sequences.
REFERENCE
             (bases 1 to 2537)
 AUTHORS
 TITLE
          NUCLEIC ACID ENCODING TGF- beta 3 AND ITS USE
          Patent: WO 8912101-A 4 14-DEC-1989;
 JOURNAL
FEATURES
                  Location/Qualifiers
    source
                  1. .2537
                  /organism="synthetic construct"
                  /mol type="mRNA"
                  /db xref="taxon:32630"
                  842. .2014
    CDS
                  /codon start=1
                  /transl table=11
                  /product="preTGF-beta1"
                  /protein id="CAA00588.1"
                  /db xref="GI:412941"
                  /translation="MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRK
                  RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                  YYAKEVTRVLMVETHNEIYDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR
                  LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                  RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                  QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT
                     893 c
                             739 g
                                     432 t
             473 a
ORIGIN
```

		79.9%; Score 956.6; DB 6; Length 2537; Similarity 88.5%; Pred. No. 2.5e-164; D: Conservative 0: Mismatches 114: Indels 24: Gaps	1.
		,	1;
Qу		ATGGCGCCTTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT	
Db	-	ATGCCGCCCTCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT	
Qу		CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	
Db		CTGACGCCTGGCCGGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	
Qу		GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	
Db	962	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	1021
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	1022	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGCCC	1081
Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCTGAG	1141
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qу	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACACAGCATATATAT	1261
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACCTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442		1501
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502		1561
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
DŁ	1562		1621
Ωŧ	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840

```
1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Db
        841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                           --GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
        901 TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
           1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
           1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
           1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
            1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
            1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Dh
RESULT 14
E00973
                                              linear PAT 29-SEP-1997
                                       RNA
                              2527 bp
LOCUS
          E00973
DEFINITION cDNA encoding human TGF-beta.
          E00973
ACCESSION
          E00973.1 GI:2169234
VERSION
          JP 1986219395-A/1.
KEYWORDS
          Homo sapiens (human)
SOURCE
         Homo sapiens
 ORGANISM
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
             (bases 1 to 2527)
REFERENCE
 AUTHORS
          Riku, M.A.D.D. and Debitsudo, B.G.
          NUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
 TITLE
 JOURNAL
          Patent: JP 1986219395-A 1 29-SEP-1986;
          GENENTECH INC
COMMENT
          OS
              human
              JP 1986219395-A/1
          PN
              29-SEP-1986
          PD
              20-MAR-1986 JP 1986064661
          PF
              22-MAR-1985 US 85
                               715142
              RIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU PC
           C12P21/00, C12N1/00, C12N5/00, C12N15/00//C12Q1/68, (C12P21/00, PC
          C12R1:91),
              (C12N1/00, C12R1:19), (C12N5/00, C12R1:91), (C12N15/00, C12R1:91);
          CC
              strandedness: Double;
          CC
              topology: Linear;
              hypothetical: No;
          CC
          CC
              anti-sense: No;
```

```
CC
            *source: tissue type=placenta and glyoblastoma; FH
                                                    Key
             Location/Qualifiers
        FH
        FT
                        842. .2014
            CDS
         FΤ
                        /product='pre TGF-beta'
         FT
            mat peptide
                        1676. .2011
         FT
                        /product='TGF-beta'
        FT
            5'UTR
                        1. .841
                        2015. .2537
        FT
            3'UTR
         FT
            stem loop
                        37. .113
         FT
            stem loop
                        2015. .2100
            polyA_site
                        2514. .2519.
FEATURES
               Location/Qualifiers
               1. .2527
   source
               /organism="Homo sapiens"
               /mol type="genomic RNA"
               /db xref="taxon:9606"
BASE COUNT
            472 a
                  888 c
                         735 g
                               432 t
ORIGIN
                   79.8%; Score 955; DB 6; Length 2527;
 Query Match
 Best Local Similarity
                   88.4%; Pred. No. 4.9e-164;
 Matches 1058: Conservative
                        0; Mismatches 115; Indels
                                               24; Gaps
                                                         1:
         Qу
          Db
Qу
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
          Db
       902 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          Db
       962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          Db
      1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTC 1081
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
QУ
          Db
      1082 TACAACAGCACCGGGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
QУ
          1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
Db
Qу
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
          1202 TATGACAAGTTCAAGCAGAGTACACACACACATATATATGTTCTTCAACACATCAGAGCTC 1261
Dh
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
QУ
          Db
      1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Qу
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
```

Db	1322		1381
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442		1501
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502		1561
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622		1675
Qу	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676		1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1778	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1837
Qу	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1838	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG	1897
Qy	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1898	GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC	1957
Qу	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 119	97
Db	1958	AAGCCCAAGGTGGAGGAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 20	14

RESULT 15 BT007245

linear PRI 13-MAY-2003 LOCUS BT007245 1173 bp mRNA DEFINITION Homo sapiens transforming growth factor, beta 1 (Camurati-Engelmann

disease) mRNA, complete cds.

ACCESSION BT007245

VERSION BT007245.1 GI:30583328

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

```
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 1173)
 AUTHORS
            Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
            Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
            Phelan, M. and Farmer, A.
  TITLE
            Cloning of human full-length CDSs in BD Creator(TM) System Donor
            vector
  JOURNAL
            Unpublished
REFERENCE
               (bases 1 to 1173)
            Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
 AUTHORS
            Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
            Phelan, M. and Farmer, A.
  TITLE
            Direct Submission
            Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
  JOURNAL
            Circle, Palo Alto, CA 94303, USA
            This CDS clone is a part of a collection of human full length
COMMENT
            expression clones generated by BD Biosciences Clontech and the
            Harvard Institute of Proteomics. Each CDS has been cloned in two
            forms: with and without stop-codon (to allow fusion with C-terminal
            tag). The CDS has been directionally cloned using BD In-Fusion(TM)
            cloning system between the Sall and HindIII sites of the pDNR-DUAL
            vector. Additional sequences in the clone: 'ACC' after SalI site
            and before 'ATG' to provide Kozak consensus sequence; 'GG' after
            last codon and before HindIII site to maintain reading frame.
            Clone distribution: http://bioinfo.clontech.com/orfclones.
FEATURES
                     Location/Oualifiers
                     1. .1173
     source
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="GH00247X1.0"
                     /clone_lib="BD Creator(TM) CDS Library derived from MGC
                     collection"
                     /lab host="DH5alpha T1 resistant"
                     /note="Vector: pDNR-Dual"
     CDS
                     1. .1173
                     /codon start=1
                     /product="transforming growth factor, beta 1
                     (Camurati-Engelmann disease)"
                     /protein id="AAP35909.1"
                     /db xref="GI:30583329"
                     /translation="MPPSGLRLLLLLLLLLLLLLVLTPGRPAAGLSTCKTIDMELVKRK
                     RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                     YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                     KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR
                     LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                     RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD'I
                     QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT
                238 a
                                            203 t
                         380 c
                                  352 g
ORIGIN
                          79.7%; Score 954.6; DB 9; Length 1173;
  Query Match
  Best Local Similarity
                          88.5%; Pred. No. 6.3e-164;
  Matches 1057; Conservative 0; Mismatches 114; Indels 24; Gaps
                                                                              1;
```

Qy	1	ATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCT	60
Db	1		60
Qу	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	61	CTGACGCCTGGCCGGCCGCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	120
Qу	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	121	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	180
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	181	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	240
Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	241	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	300
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	301	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	360
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	361	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	420
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	421	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	480
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	481	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	540
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	541	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	600
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	601	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	660
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	661	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	720
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	721	ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	780
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	781	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	834
Qy	841	${\tt AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC}$	900

Db	835		876
Qу	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	877	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	936
Qу	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	937	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	996
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	997	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG	1056
Qy	1081	GCGCCGTGCTGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1057	GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC	1116
Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCT 1195	
Db	1117	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCT 1171	

Search completed: October 27, 2003, 18:34:42 Job time: 4678.52 secs

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 359.617 Seconds

(without alignments)

8985.201 Million cell updates/sec

Title: US-10-017-372E-8

Perfect score: 1197

Sequence: 1 atggcgccttcggggctgcg.....gttcctgcaagtgcagctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

```
/SIDS1/gcgdata/geneseg/genesegn-emb1/NA1981.DAT: *
3:
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4:
    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5:
    /SIDS1/gcgdata/geneseg/genesegn-emb1/NA1984.DAT: *
6:
    /SIDS1/gcgdata/geneseg/genesegn-emb1/NA1985.DAT: *
    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
7:
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
8:
9:
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10:
    /SIDS1/gcgdata/geneseg/genesegn-embl/NA1989.DAT: *
11:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
14:
15:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT: *
16:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT: *
17:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20:
     /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query				
No.	Score	_	Length	DB	ID	Description
1	1135.8	94.9	1326	24	AAD22696	Porcine transformi
2	958.2	80.1	2742	22	AAI58342	Human polynucleoti
3	956.6	79.9	1559	13	AAQ20289	Sequence encoding
4	956.6	79.9	1561	11	AAQ03268	Simian transformin
5	956.6	79.9	1821	12	AAQ13392	Human pro-TGF-beta
6	956.6	79.9	2537	7	AAN60972	Sequence encoding
7	956.6	79.9	2537	11	AAQ03301	cDNA encoding huma
8	956.6	79.9	2537	11	AAQ02814	Sequence of pre-TG
9	956.6	79.9	2537	17	AAT15720	Pre-transforming g
10	955	79.8	2527	25	ABQ76674	Androgen receptor
11	955	79.8	2537	15	AAQ56923	Human pre-TGF-beta
12	953.4	79.6	1560	9	AAN81084	Coding sequence of
13	953.4	79.6	1560	11	AAQ03508	Simian Transformin
14	951.8	79.5	2537	19	AAV52933	Human pre-transfor
15	945.2	79.0	1176	25	ABV75391	TGFB1 Arg25Pro pol
16	943.6	78.8	1176	24	ABZ35738	Human TGF beta 1 p
17	943.6	78.8	1176	24	ABX09981	Human TGFbetal DNA
18	943.6	78.8	1176	24	ABV78162	Human TGF beta 1 D
19	943.6	78.8	1176	24	ABL91703	Human polynucleoti
20	943.6	78.8	1176	25	ABV75392	TGFB1 Arg25Pro pol
21	943.6	78.8	1303	11	AAQ09317	Monkey transformin
22	943.6	78.8	2745	16	AAT05876	cDNA encoding tran
23	943.6	78.8	2745	22	AAH28216	Nucleotide sequenc

```
4105 15 AAQ55624
  24
       943.6
               78.8
                                                        TGFbeta1 5'-UTR-CD
                                                        Human transforming
  25
       940.4
               78.6
                      1571
                          11 AAQ03269
                      1569 9 AAN81085
                                                       Coding sequence of
  26
       938.8
               78.4
  27
       937.2
               78.3
                      1569 11 AAO03509
                                                        Human Transforming
  28
       926.2
               77.4
                      1561
                          11 AAO04908
                                                        Sequence encoding
                                                        TGF-beta 1/beta 2
  29
         923
               77.1
                      1561
                          13 AAO29177
                                                        TGF-beta 1. Homo
  30
       884.8
               73.9
                      1565 13 AAQ29178
  31
         803
               67.1
                      2208 13 AAO20291
                                                        Sequence encoding
  32
       801.4
              67.0
                      2206
                           11 AAO03510
                                                        Human Transforming
  33
       801.4
              67.0
                      2207
                           11 AAQ03511
                                                        Hybrid transformin
                           11 AAQ05127
                                                        Human TGF-Beta1/TG
  34
       799.8
              66.8
                      2207
  35
       788.4
               65.9
                      2217 10 AAN90768
                                                        Sequence of human
               65.3
                                                        Simian-human hybri
  36
       782.2
                      2200 16 AAT04115
 37
       778.4
               65.0
                      2765 22 AAI60128
                                                        Human polynucleoti
               56.7
                      834 12 AAQ12192
                                                        Sequence encoding
  38
       678.8
               56.3
                      2773 23 AAS84421
                                                        DNA encoding novel
c 39
       673.4
         654
               54.6
                      1376
                           24
                               ABK90341
                                                        DNA encoding LAP-m
  40
       652.4
               54.5
                      1389 24 ABK90344
                                                        DNA encoding LAP-h
  41
       588.2
                                                        DNA encoding mIFNB
               49.1
                      1352 24 ABK90342
  42
                                                        DNA encoding huIFN
  43
       586.6
               49.0
                     1350 24 ABK90343
               43.0
                      875 23 AAS70979
                                                        DNA encoding novel
  44
       514.8
         344
               28.7
                      489 24 ABL99528
                                                        Target canine gene
  45
```

ALIGNMENTS

```
RESULT 1
AAD22696
     AAD22696 standard; cDNA; 1326 BP.
ID
XX
AC
     AAD22696;
XX
DT
     26-FEB-2002 (first entry)
XX
     Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.
DE
XX
KW
     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW
KW
     diabetes mellitus; sarcoidosis; psoriasis; dermatological; ss.
XX
OS
     Sus scrofa.
XX
FH
                      Location/Qualifiers
     Key
FT
                      16..1188
     CDS
FT
                      /*taq≈ a
FT
                      /product= "Porcine TGF-beta1 mutant protein"
XX
PN
     WO200181404-A2.
XX
PD
     01-NOV-2001.
XX
     20-APR-2001; 2001WO-US12980.
PF
XX
PR
     20-APR-2000; 2000US-199014P.
XX
```

```
PA
    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PΙ
    Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
DR
    WPI; 2002-026155/03.
DR
    P-PSDB: AAE13596.
XX
PT
    Composition for treating autoimmune diseases e.g. inflammatory bowel
PT
    disease in humans, comprises vector containing transforming growth
PT
    factor-beta under the control of inducible promoter
XX
PS
    Claim 1; Fig 1; 78pp; English.
XX
CC
    The invention relates to a composition containing a vector comprising a
CC
    gene encoding a regulatory transcription factor under the control of a
CC
    promoter encoding a transforming growth factor-beta (TGF-beta). The
CC
    vector is useful for expressing TGF-beta, such as TGF-betal, TGF-beta2
CC
    or TGF-beta3, its variants or homologues, by transfecting a cell which
CC
    is part of a host suspected of having an autoimmune disease, especially
CC
    inflammatory bowel disease (IBD), under conditions such that the
CC
    polypeptide encoded by the nucleic acid sequence in the vector is
CC
    expressed. The vector is delivered using a delivery system. The delivery
CC
    of the vector results in substantial elimination of symptoms of the
CC
    autoimmune disease and increased production of IL-10 by the host. The
CC
    composition is useful for treating various diseases with an autoimmune
    component such as multiple sclerosis, rheumatoid arthritis, systemic
CC
    lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC
    and psoriasis, and also for assaying the expression of a gene in a cell.
CC
CC
    The vector is further useful for screening of the effect of test
    compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC
CC
    The present sequence is a cDNA encoding porcine TGF-betal mutant.
XX
    Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;
SO
                     94.9%; Score 1135.8; DB 24; Length 1326;
 Query Match
 Best Local Similarity
                     97.8%; Pred. No. 3.7e-231;
 Matches 1171; Conservative
                          0; Mismatches
                                          2; Indels
                                                     24; Gaps
          Qу
            Db
         61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
            76 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 135
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
            136 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTCGCC 195
Db
        Qу
           Db
        196 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGTACTGGCTCTT 255
        241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
            256 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 315
Db
```

Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	316	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	375
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	376	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	435
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	436	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	495
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	496	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	555
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	556	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	615
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	616	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	675
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	676	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	735
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	736	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	795
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCGCGAGACTAC	840
Db	796	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGA	849
Qу	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	850		891
Qy	901	TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	892	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	951
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	952	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1011
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1012	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1071
Qy	1081	GCGCCGTGCTGCGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1072	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1131

```
1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
              1132 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1188
Db
RESULT 2
AAI58342
    AAI58342 standard; cDNA; 2742 BP.
XΧ
AC
    AAI58342;
XX
DT
    22-OCT-2001 (first entry)
XX
DE
    Human polynucleotide SEQ ID NO 545.
XX
KW
    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
    peripheral nervous system; neuropathy; central nervous system; CNS;
KW
    Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW
KW
    amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW
     chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW
     leukaemia; ss.
XX
OS
    Homo sapiens.
XX
PN
    WO200153312-A1.
XX
PD
    26-JUL-2001.
XX
     26-DEC-2000; 2000WO-US34263.
PF
XX
PR
     21-JAN-2000; 2000US-0488725.
PR
     25-APR-2000; 2000US-0552317.
PR
     09-JUL-2000; 2000US-0598042.
PR
     19-JUL-2000; 2000US-0620312.
PR
     03-AUG-2000; 2000US-0653450.
     14-SEP-2000; 2000US-0662191.
PR
     19-OCT-2000; 2000US-0693036.
PR
PR
     29-NOV-2000; 2000US-0727344.
XX
PΑ
     (HYSE-) HYSEQ INC.
XX
     Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PΙ
ΡI
     Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y,
                                                          Zhang J;
     Zhao QA, Zhou P, Goodrich R, Drmanac RT;
PΙ
XX
DR
     WPI; 2001-442253/47.
     P-PSDB; AAM39186.
DR
XX
PT
     Novel nucleic acids and polypeptides, useful for treating disorders
PT
     such as central nervous system injuries -
XX
     Claim 1; SEQ ID NO 545; 10078pp; English.
PS
XX
CC
     The invention relates to human nucleic acids (AAI57798-AAI61369) and
     the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC
     immunosuppressant and cytostatic activity. The polynucleotides are useful
CC
CC
     in gene therapy. A composition containing a polypeptide or polynucleotide
```

```
CC
   of the invention may be used to treat diseases of the peripheral nervous
CC
    system, such as peripheral nervous injuries, peripheral neuropathy and
CC
    localised neuropathies and central nervous system diseases, such as
CC
   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC
   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC
   utilisation of the activities such as: Immune system suppression,
CC
   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC
    and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC
    assays for receptor activity, arthritis and inflammation, leukaemias and
CC
    C.N.S disorders.
CC
   Note: The sequence data for this patent did not form part of the printed
CC
    specification.
XX
SO
   Sequence 2742 BP; 526 A; 938 C; 799 G; 479 T; 0 other;
 Query Match
                    80.1%; Score 958.2; DB 22; Length 2742;
 Best Local Similarity
                    88.6%; Pred. No. 1.6e-193;
 Matches 1060; Conservative
                         0; Mismatches 113; Indels
                                                 24; Gaps
                                                           1;
         Qу
           Db
        61 CTGACGCCTGGCCGGCCGCCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           902 CTGACGCCTGGCCGGCCGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
           1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
Db
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCCTGCTGAGGCTC 480
Qу
           1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Db
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
           1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
Db
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qу
```

```
Db
      1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
Qу
          Db
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qу
          Db
      1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACTGCAAGTGGACATCAACGGGTTCACT 1561
QУ
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
           1562 ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
Db
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
           1622 ATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Db
       841 AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                        Db
                     ----GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
           1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
           1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
Qу
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
           Dh
      1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
       1081 GCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
           1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Db
RESULT 3
AA020289
   AAO20289 standard; cDNA; 1559 BP.
ΙD
XX
AC
   AAQ20289;
XX
DT
   25-MAR-2003 (updated)
DT
   16-APR-1992 (first entry)
XX
DE
   Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW
   Hypertension therapy; hypotensive agent; blood pressure modulator;
KW
   SS.
```

XX

```
OS
    Monkey.
XX
                 Location/Oualifiers
FΗ
    Key
FT
    CDS
                  262..282
FT
                  /*tag=a
FT
    sig peptide
                  283..324
                  /*tag=b
FT
                  325..1098
FT
    CDS
FT
                  /*tag=c
FT
    mat peptide
                  1099..1436
FT
                  /*tag= d
XX
PN
    WO9119513-A.
XX
PD
    26-DEC-1991.
XX
PF
    20-JUN-1991;
               91WO-US04449.
XX
PR
    20-JUN-1990; 90US-0541221.
XX
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA
XX
PΙ
    Oleson FB, Comereski CR;
XX
DR
    WPI; 1992-024199/03.
    P-PSDB; AAR20124.
DR
XX
PΤ
    Use of transforming growth factor (TGF)-beta and their
PT
    antagonists - for modulating blood pressure, for treating
PT
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CC
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-betal/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
    Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;
 Query Match
                      79.9%; Score 956.6; DB 13; Length 1559;
 Best Local Similarity 88.5%; Pred. No. 3.3e-193;
 Matches 1059; Conservative 0; Mismatches 114; Indels
                                                      24; Gaps
                                                                  1;
Qу
          Db
         61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
            Db
        321 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 380
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Ov
```

Db	381		440
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	500
QУ		TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	
Db		TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGAGTGCGGAGCCCGAACCGGAG	
QУ		GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	
Db		GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	
QУ	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	621	TATGACAAGTTCAAGCAGAGCACACACACACATATATATGTTCTTCAACACATCAGAGCTC	680
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	681	CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	740
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	741	AAGTTAAAAGTCGAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	800
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	801	TACCTCAGCAACCGGCTGCTGGCGCCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	860
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	861	ACCGGAGTTGTGCGCCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	920
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	921	GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	981	ACCGGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1040
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1041	ATGGCCACCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA	1094
Qу	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1095	GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	1136
Qу	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1137	TGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1196
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020

```
1197 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG 1256
Db
        1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGTCGGCG 1080
Qy
            1257 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1316
Db
        1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGCCGC 1140
Qу
            1317 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1376
Db
        1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
            1377 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1433
Dh
RESULT 4
AAQ03268
    AAQ03268 standard; DNA; 1561 BP.
ID
XX
AC
    AAQ03268;
XX
DT
    25-MAR-2003
                (updated)
DT
    12-AUG-1990 (first entry)
XX
    Simian transforming growth factor-beta cDNA.
DE
XX
    Transforming growth factor-beta; psoriasis; TGF-beta; ss.
KW
XX
OS
    Monkey.
XX
FΗ
                  Location/Qualifiers
    Key
                   283..324
    sig peptide
FT
                   /*tag=a
FT
                   1096..1431
FT
    mat_peptide
FT
                   /*tag=b
                   /product=human transforming growth factor-beta
FT
XX
PN
    EP353772-A.
XX
PD
    07-FEB-1990.
XX
                 89EP-0114458.
PF
    04-AUG-1989;
XX
    05-AUG-1988;
                88US-0229133.
PR
XX
    (ONCO ) ONCOGEN LP.
PΑ
XX
PΙ
    Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
    WPI; 1990-038499/06.
DR
DR
    P-PSDB; AAR03743.
XX
    Inhibition of proliferation of epidermal cells -
PT
    used to treat psoriasis by contacting cells with compositions
PT
    containing transforming growth factor-beta.
PT
XX
    Disclosure; fig 1; 20pp; English.
PS
```

```
XX
   TGF-beta may be used in the treatment of hyperplasia
CC
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
   induced phenomena. See also AAQ03269 and AAR03750.
CC
   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ
   Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
 Query Match
                  79.9%; Score 956.6; DB 11; Length 1561;
 Best Local Similarity 88.5%; Pred. No. 3.3e-193;
 Matches 1059; Conservative
                       0; Mismatches 114;
                                      Indels
                                              24; Gaps
                                                       1;
        Qу
          Db
       61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          Db
       322 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 381
Qy
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
          382 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 441
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          442 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 501
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          502 TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGACTGCGGAGCCCGAACCGGAG 561
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
          562 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 621
Db
Qу
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
          622 TATGACAAGTTCAAGCAGAGCACACACACACATATATATGTTCTTCAACACATCAGAGCTC 681
Db
Qу
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
          Db
       682 CGAGAAGCAGTACCTGAACCTGTGTTGCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 741
Qy
       481 AAGTTAAAAGTGGAGCACCTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
          742 AAGTTAAAAGTGGAGCAGCATGTGGAGCTGTACCAGAAATTCCAGCAACAATTCCTGGCGA 801
Db
Qу
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
          802 TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC 861
Db
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 660
Qу
          862 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 921
Db
```

```
QУ
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
          Db
       922 GCCCACTGCTCCTGTGACAGCAAAGATAACACTGCAAGTGGACATCAACGGGTTCACT 981
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
           Db
       982 ACCGGCCGCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1041
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          1042 ATGGCCACCCCACTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA----- 1095
Db
       841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                        Db
       1096 -----GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 1137
QУ
       901 TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
          1138 TGCTGCGTGCGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1197
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1198 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG 1257
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
          1258 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1317
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          Db
       1318 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1377
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
       1378 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1434
RESULT 5
ID
   AAQ13392 standard; DNA; 1821 BP.
XX
AC
   AAQ13392;
XX
DT
   20-NOV-1991 (first entry)
XX
DΕ
   Human pro-TGF-beta 1 gene.
XX
KW
   Osteogenetic; tumoricidal; ss.
XX
OS
   Homo sapiens.
XX
FH
               Location/Qualifiers
   Key
FT
   CDS
               512..1684
FT
               /*tag= a
FT
               512..598
   sig_peptide
FT
                /*tag= b
```

FT

misc RNA

599..1684

```
/*tag= c
FT
                /note= "pro-TGF-beta 1"
FT
   mat peptide
                1346..1684
FT
                /*tag= e
FT
                /note= "TGF-beta 1"
XX
PN
   JP03180192-A.
XX
PD
   06-AUG-1991.
ХX
PF
   07-DEC-1989;
               89JP-0318243.
XX
PR
   07-DEC-1989;
              89JP-0318243.
XX
PA
    (KIRI ) KIRIN BREWERY KK.
XX
DR
   WPI; 1991-271579/37.
   P-PSDB; AAR13813.
DR
XX
PT
   Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT
   preparing DNA chain contq. base sequence coding for human
PT
   pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS
   Claim 1; Fig 1; 16pp; Japanese.
XX
CC
   The DNA sequence encodes human prepro-TGF-beta 1 which can be
CC
   produced by recombinant methods, it has osteogenetic and
CC
   tumoricidal activity.
XX
SO
   Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;
 Query Match
                    79.9%;
                         Score 956.6; DB 12; Length 1821;
 Best Local Similarity
                   88.5%; Pred. No. 3.3e-193;
 Matches 1059; Conservative
                        0; Mismatches 114;
                                         Indels
                                                24; Gaps
                                                           1;
         Qу
           Db
       Qу
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
           Db
       572 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 631
Qу
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
          Db
       632 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTGGCC 691
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           Db
       692 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 751
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          752 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGACTGCAGAACCGGAGCCCGAGCCTGAG 811
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
QУ
```

FT

Db	812	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	871
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	872	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	931
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	932	CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	991
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	992	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1051
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1052	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1111
Qy		ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	
Db		ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	
Qy		GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	
Db		GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	
Qy		TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	
Db		ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	
QУ		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	
Db		ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCCCGA	
QУ		AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	
Db		TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	
Qy Db		TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	
Qy		GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	
Db			
Qy		GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	
Db			
Qy	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db			
Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 119	97
Db	1628	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 168	34

```
RESULT 6
AAN60972
     AAN60972 standard; cDNA; 2537 BP.
XX
AC
     AAN60972;
XX
DT
     31-OCT-2002 (updated)
DT
     28-OCT-1991 (first entry)
XX
DE
     Sequence encoding preTGF-beta.
XX
KW
     Transforming growth factor beta; cancer; wound healing.
XX
OS
     Unidentified.
XX
FH
     Key
                     Location/Qualifiers
FT
     misc structure 37..113
FT
                     /*tag= a
FT
                     /note= "Sequence can form stable hairpin loops"
FT
     CDS
                     842..2014
FT
                     /*tag= b
FT
     mat peptide
                     1676..2011
FT
                     /*tag= c
XX
PN
     EP200341-A.
XX
PD
     10-DEC-1986.
XX
PF
     21-MAR-1986;
                    86EP-0302112.
XX
PR
     22-MAR-1985;
                    85US-0715142.
     13-MAR-1987;
PR
                    87US-0025423.
XX
PΑ
     (GETH ) GENENTECH INC.
XX
PΙ
     Derynck RMA;
XX
     WPI; 1986-326875/50.
DR
DR
     P-PSDB; AAP61468.
XX
PΤ
     TGF-beta prodn. from transformed hosts - useful esp. for treating
PT
     wounds (J6 2/9/86).
XX
PS
     Disclosure; Fig 1b; 26pp; English.
XX
CC
     The gene product is known to stimulate cell proliferation and
CC
     inhibit anchorage-dependent growth of a variety of human cancer cell
CC
     lines, it is esp. useful in treatment of burns and the promotion of
CC
     surface and internal wound healing. TGF-beta may be expressed from a
     transformed CHO cell line.
CC
     (Updated on 31-OCT-2002 to add missing OS field.)
CC
XX
SO
     Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                          79.9%; Score 956.6; DB 7; Length 2537;
  Query Match
```

		Similarity 88.5%; Pred. No. 3.5e-193; 9; Conservative 0; Mismatches 114; Indels 24; Gaps	1;
Qу	1	ATGGCGCCTTCGGGGCTGCTGCCGCTGCTGCTGCTGCTGCT	60
Db	842		901
Qу	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	902	CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	961
Qу	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	962		1021
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	1022	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCCCGAGGCCGTGCTCGCCCTG	1081
Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	1141
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1501
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1561
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840

```
Qу
        841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
                          Db
       1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
        901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
           Db
       1718 TGCTGCGTGCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
           1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Dh
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
           1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
           1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           Db
       1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 7
AA003301
    AAQ03301 standard; DNA; 2537 BP.
XX
AC
   AAQ03301;
XX
DT
    25-MAR-2003
              (updated)
DT
    05-AUG-1990 (first entry)
XX
    cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
DΕ
DΕ
XX
KW
    Transforming growth factor-beta-1 (TGF-beta-1);
    neoplastic cell line inhibition;
KW
    EGF-potentiated anchorage-independent growth;
KW
XX
OS
    Homo sapiens.
XX
                 Location/Qualifiers
FH
    Key
FT
    CDS
                 842..2014
FT
                 /*tag= a
                 1676..2011
FT
    mat peptide
FT
                 /*tag=b
FT
    misc difference 37..113
FT
                 /*tag= c
FT
                 /note="stable hairpin loops"
FT
    misc feature
                 2015..2100
FT
                 /*tag= d
                 /note="G-C rich sequence
FT
FT
                  and a downstream TATA-like sequence"
```

1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675

Db

```
PN
    US4886747-A.
XX
PD
    12-DEC-1989.
XX
PF
    13-MAR-1987:
              87US-0025423.
XX
PR
    13-MAR-1987; 87US-0025423.
XX
PA
    (GETH ) GENENTECH INC.
XX
PI
    Derynck RMA, Goeddel DV;
XX
DR
    WPI; 1990-051338/07.
    P-PSDB; AAR05258.
DR
XX
PT
    Nucleic acid encoding transforming growth factor-beta -
PΤ
    cloned into expression vectors for expression in eukaryotic host
PT
    cells for therapeutic use
XX
PS
    Disclosure; Fig 1b; 28pp; English.
XX
CC
    It was obtained by an analysis of several overlapping cDNAs and gene
CC
    fragments, leading to the detn. of a continuous sequence corresp. to the
    TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
CC
CC
    encode biologically active transforming growth factor (TGF-beta),
CC
    operably linked to DNA that encodes a secretory leader (SL). It, or a
CC
    nucleic acid capable of hybridising with it, can also be labelled and
    used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
CC
CC
    proteins.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Query Match
                    79.9%; Score 956.6; DB 11; Length 2537;
 Best Local Similarity
                    88.5%; Pred. No. 3.5e-193;
 Matches 1059; Conservative
                        0; Mismatches 114; Indels 24; Gaps
                                                            1:
         Qу
           Db
       61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           Db
       902 CTGACGCCTGGCCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qy
           Db
       962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
QУ
           Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141
Db
```

XX

Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142		1201
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACACACATATATATGTTCTTCAACACATCAGAGCTC	1261
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACCACGAGCAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1501
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502		1561
Qу	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1675
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676		1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1778	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1837
Qy	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1838	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG	1897
Qу	1081	GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140
Db	1898	GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC	1957

```
Qу
        1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
              Db
        1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 8
AAQ02814
    AAQ02814 standard; cDNA; 2537 BP.
XX
AC
    AAQ02814;
XX
DT
    25-MAR-2003 (updated)
DT
    31-OCT-2002 (updated)
DT
    31-MAY-1989 (first entry)
XX
DE
    Sequence of pre-TGF-betal cDNA.
XX
KW
    Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW
    inhibition.
XX
OS
    Homo sapiens.
XX
FH
                    Location/Qualifiers
    Key
FT
                    842..2011
    CDS
FT
                    /*taq=a
FT
                    /label=pre-TGF beta 1
FT
    CDS
                    1677..2011
FT
                    /*tag=b
FT
                    /label=mature TGF-beta 1
                    2015..2092
FT
    GC_signal
FT
                    /*tag= c
FT
                    2093..2099
    misc_feature
FT
                    /*tag= d
                    /label=TATA-like sequence
FT
FT
                    37..113
    stem loop
FT
                    /*tag= e
FT
                    863..911
    misc_feature
FT
                    /*tag= f
                    /label=hydrophobic domain
FT
XX
    WO8912101-A.
PN
XX
    14-DEC-1989.
PD
XX
ΡF
    08-JUN-1988;
                  88WO-US01945.
XX
PR
    08-JUN-1988;
                   88WO-US01945.
XX
     (GETH ) GENENTECH INC.
PA
XX
    Dernyck RMA, Goeddel DV;
PΙ
XX
    WPI; 1990-007474/01.
DR
    P-PSDB; AAR04034.
DR
XX
    Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT
PT
    probe, or to produce TGF beta 3, for growth inhibition of certain normal
```

```
and neoplastic cells, eq A549.
XX
PS
   Disclosure; Fig. 1b; 61pp; English.
XX
CC
   Sequence encodes the 390 amino acid (AA) precursor transforming growth
    factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
CC
CC
    the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
   potential secondary structure. The TATA-like sequence in the 3' untrans-
CC
CC
    lated region of the gene is presumably a polyadenylation signal. Mature
CC
    TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
CC
    cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic
CC
    acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a
CC
   probe or to produce TGF-beta 3 for inhibition of growth of normal and
CC
   neoplastic cells.
    (Updated on 31-OCT-2002 to add missing OS field.)
CC
CC
    (Updated on 25-MAR-2003 to correct PR field.)
    (Updated on 25-MAR-2003 to correct PI field.)
CC
XX
SQ
   Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Query Match
                    79.9%; Score 956.6; DB 11; Length 2537;
                    88.5%; Pred. No. 3.5e-193;
 Best Local Similarity
 Matches 1059: Conservative
                        0: Mismatches 114: Indels
                                                            1;
                                                 24; Gaps
         Qу
           Db
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           Db
       902 CTGACGCCTGGCCGCCGGCCGGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
           1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
      Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           Db
       1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
       361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
                           Db
       1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
           1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Dh
       481 AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qv
```

PT

```
Db
      1322 AAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
Qу
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
          1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
Db
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 660
QУ
          Dh
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
Qу
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
          Db
      1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACTGCAAGTGGACATCAACGGGTTCACT 1561
Qу
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
           Db
      1562 ACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          Db
      1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
       841 AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                       1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAC 1717
Dh
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
          1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
       961 GAACCCAAGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1778 GAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTACATTTGGAGCCTG 1837
Dh
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
          1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
      1081 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          Db
      1898 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Qу
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
          Db
      1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 9
   AAT15720 standard; cDNA; 2537 BP.
ID
XX
AC
   AAT15720;
ХX
DT
   25-MAR-2003 (updated)
```

24-JUL-1997 (revised)

25-JAN-1980 (first entry)

DT

DT

```
XX
DE
     Pre-transforming growth factor beta 1 cDNA.
XX
KW
     transforming growth factor beta 1; wound healing;
KW
     recombinant production; ss.
XX
OS
     Homo sapiens.
XX
FH
     Key
                     Location/Qualifiers
FT
     5'UTR
                     1..841
FΤ
                     /*taq=a
FT
     misc_feature
                     37..113
FT
                     /*tag= b
FT
                      /note= "GC-rich region forms stable hairpin loops;
FT
                              similar to structural organisation of c-myc RNA,
FT
                              could play role in mRNA stability or in
FT
                              regulation of transcription"
     CDS
FT
                      842..2014
                      /*tag= c
FT
                      /product= pre-TGF_beta_1
FT
                      1676..2011
FT
     mat peptide
FT
                      /*tag= d
FT
                      /product= mature TGF beta 1
FT
     repeat_region
                      2015..2100
FT
                      /*taq= e
                      /note= "GC-rich region; possibly responsible for the
FT
FT
                              fact 3'UTR of mRNA could not be cloned as cDNA;
                              may be important for transcription efficiency"
FT
FT
                      2019..2023
     repeat_unit
                      /*tag= f
FT
                      2094..2100
FT
     TATA signal
FT
                      /*tag= g
                      /note= "TATA-like sequence; no evidence that this
FT
                              functions a promoter"
FT
FT
     polyA signal
                      2514..2520
FT
                      /*tag= h
                      2529..2536
FT
     misc_signal
FT
                      /*taq= i
                      /note= "consensus sequence immediately precedes
FT
                              polyA-tail (Benoist et al)"
FT
XX
     US5482851-A.
PN
XX
PD
     09-JAN-1996.
XX
PF
     05-NOV-1993;
                     93US-0147364.
XX
                     87US-0025423.
PR
     13-MAR-1987;
     22-MAR-1985;
PR
                     85US-0715142.
     04-AUG-1989;
                     89US-0389929.
PR
PR
     04-MAR-1992;
                     92US-0845893.
                    93US-0147364.
PR
     05-NOV-1993;
XX
PA
     (GETH ) GENENTECH INC.
XX
PΙ
     Derynck RMA, Goeddel DV;
XX
```

```
WPI; 1996-076891/08.
   P-PSDB; AAR90827.
DR
XX
PT
   New recombinant human transforming growth factor-beta prods. - produced
PT
   using Chinese hamster ovary cells, for use in diagnostic applications
РТ
   or in therapy
XX
PS
   Example 3; Fig 1; 26pp; English.
XX
CC
   The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
CC
   The nucleotide sequence was obtd. by an analysis of several overlapping
CC
   cDNAs and gene fragments. The DNA is useful for the recombinant
   production of TGF beta 1, which can be used in, e.g. wound healing.
CC
CC
   (Revised entry submitted to correct sequence analysis breakdown.)
CC
   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
   Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Ouery Match
                   79.9%; Score 956.6; DB 17; Length 2537;
 Best Local Similarity
                   88.5%; Pred. No. 3.5e-193;
 Matches 1059; Conservative
                       0; Mismatches 114;
                                         Indels
                                                24; Gaps
                                                          1:
         Qу
          Db
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          902 CTGACGCCTGGCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          1082 TACAACAGCACCGCGACCGGGTGGCCGGGGAGATGCAGAACCGGAGCCCGAGCCTGAG 1141
Db
Ov
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
          1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
Db
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
          1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Db
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
          1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
Db
```

DR

```
Qу
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
          Db
      1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 660
Qу
          Db
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qу
          Db
      1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 1561
       721 TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
           Db
      1562 ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
       781 ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Dh
       841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                        1676 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
Qу
       901 TGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
          1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Dh
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          Db
      1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
          1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
      1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
          1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
Qу
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
          1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Db
RESULT 10
ABQ76674
   ABQ76674 standard; DNA; 2527 BP.
XX
AC
   ABQ76674;
XX
DT
   26-MAR-2003 (first entry)
XX
DE
   Androgen receptor signalling pathway-associated DNA E00973.
XX
   Androgen receptor; transactivation; modulator; Smad3; Smad4; Akt; TGF-B;
KW
```

```
KW
    signal transduction pathway; transforming growth factor-B; phosphatase;
KW
    tensin; cytostatic; antiproliferative; cellular proliferation; cancer;
KW
    E00973; ds.
XX
OS
    Synthetic.
XX
ΡN
    WO200282081-A2.
XX
ÞΠ
    17-OCT-2002.
XX
PF
    05-APR-2002; 2002WO-US11086.
XX
PR
    06-APR-2001; 2001US-282266P.
    13-MAR-2002; 2002US-365060P.
PR
XX
PA
    (UYRP ) UNIV ROCHESTER.
XX
PΙ
    Chang C;
XX
DR
    WPI; 2003-046871/04.
XX
    Modulating androgen receptor activity, by administering a compound that
PΤ
PT
    modulates receptor activity, inhibits receptor-signal transduction
РΤ
    pathway/receptor-coactivator interaction or changes amount or receptor
PΤ
XX
PS
    Disclosure; Page 225-226; 302pp; English.
XX
CC
    This invention describes a novel method for modulating androgen receptor
CC
    activity or androgen receptor-mediated transactivation activity in a
CC
    cell. The method involves administering a compound which causes
CC
    modulation of the androgen receptors activity and the inhibition of
CC
    interaction between the receptor and a protein involved in a signal
CC
    transduction pathway. The compound also inhibits the interaction between
CC
    the androgen receptor and a protein selected from Smad3, Smad4, Akt,
CC
    transforming growth factor (TGF)-B and phosphatase and tensin homologues
CC
    deleted on chromosome 10 (PTEN) or their fragments. The compounds of the
CC
    invention have cytostatic and antiproliferative activity. The obtained
CC
    composition is useful for treating any disease, where uncontrolled
CC
    proliferation or cellular proliferation occurs such as cancer, e.g.
CC
    prostate cancer. This sequence represents the androgen receptor
CC
    transactivation signalling pathway modulator E00973 described in
CC
    the method of the invention.
ХX
SO
    Sequence 2527 BP; 472 A; 888 C; 735 G; 432 T; 0 other;
 Query Match
                       79.8%; Score 955; DB 25; Length 2527;
 Best Local Similarity
                       88.4%; Pred. No. 7.6e-193;
 Matches 1058; Conservative
                            0; Mismatches 115;
                                                 Indels
                                                         24; Gaps
                                                                     1;
          Qу
            Db
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
            Db
         902 CTGACGCCTGGCCCGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
```

Qy	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	962		1021
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	1022	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGAGGCCGTGCTCGCCCTC	1081
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	1141
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1501
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1561
QУ	721	TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622	ATGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1675
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676		1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777

```
961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
            1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
            1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Qу
            1898 GCGCCGTGCTGCGTGCCGCAGGCGCTGCAGCCCCATCGTGTACTACGTGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Oy
            1958 AAGCCCAAGGTGGAGGAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Dh
RESULT 11
AAQ56923
ID
    AAQ56923 standard; cDNA; 2537 BP.
XX
AC
    AAO56923;
XX
DT
    25-MAR-2003 (updated)
DT
    09-JUL-1994 (first entry)
XX
    Human pre-TGF-beta-1.
DE
XX
    TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW
    transforming growth factor beta-3; recombinant; wound healing;
KW
KW
    vulnerary; ss.
XX
    Homo sapiens.
OS
XX
    Key
                  Location/Qualifiers
FH
                 47..113
    misc_structure
FT
FT
                  /*tag= a
                  /note= "possible hairpin loop region"
FT
FT
                  842..2014
    CDS
                  /*tag= b
FT
                  1676..2011
FT
    mat peptide
FT
                  /*tag= c
                  2515..2521
FT
    polyA signal
FT
                  /*taq= d
XX
ΡN
    US5284763-A.
XX
PD
    08-FEB-1994.
XX
PF
    04-MAR-1992;
                 92US-0845893.
XX
PR
    22-MAR-1985;
                 85US-0715142.
                 87US-0025423.
PR
    13-MAR-1987;
    04-AUG-1989;
                 89US-0389929.
PR
    04-MAR-1992;
                 92US-0845893.
PR
XX
PA
    (GETH ) GENENTECH INC.
```

```
XX
   Derynk RMA, Goeddel DV;
ΡI
XX
DR
   WPI: 1994-056343/07.
DR
    P-PSDB; AAR46227.
XX
   Nucleic acid sequences encoding transforming growth factor-beta -
PT
    diagnostic probes, and for use in therapeutics
PT
XX
PS
   Disclosure; Fig 1b; 25pp; English.
XX
    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC
CC
   pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC
    corresponding amino acid sequences were determined (AAR46227-29,
    respectively). A genomic fragment corresponding to a human TGF-
CC
CC
    beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
    determined (AAR46230). The sequences have been used in the
CC
    construction of vectors for the expression of recombinant TGF-
CC
CC
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
    Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
SO
 Query Match
                    79.8%; Score 955; DB 15; Length 2537;
 Best Local Similarity
                    88.4%; Pred. No. 7.7e-193;
                        0; Mismatches 115; Indels
 Matches 1058; Conservative
                                                 24;
                                                    Gaps
                                                           1;
         Qу
           Db
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           902 CTGACGCCTGGCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
Db
       181 AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Ov
           1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGTGCCCGAGGCCGTGCTCGCCCTG 1081
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           Db
       1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACGGGAGCCCGAGCCTGAG 1141
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
                           1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261
Db
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
```

```
1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321
Db
Qу
       481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
          Db
      1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qу
          1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441
Db
       601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
Qу
          Db
      1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 1501
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qу
          1502 GCCCACTGCTCCTGTGACAGCAGGGATAACACTGCAAGTGGACATCAACGGGTTCACT 1561
Db
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
           1562 ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621
Db
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Db
       841 AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
QУ
                       -----GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
          1718 TGCTGCGTGCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
Db
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACACCCGGGCGCGTCGGCG 1080
Qу
          1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1897
Db
      1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
          1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
      1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
```

```
RESULT 12
AAN81084
ID AAN81084 standard; cDNA; 1560 BP.
XX
AC AAN81084;
XX
```

```
DT
    25-MAR-2003 (updated)
DT
    09-OCT-1990 (first entry)
XX
DE
    Coding sequence of simian transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS
    Cercopithecus aethiops.
XX
FH
    Key
                  Location/Qualifiers
FT
    CDS
                  261..1433
FT
                  /*tag=a
FT
    sig_peptide
                  282..323
FT
                  /*tag=b
                  1095..1433
FT
    mat peptide
FT
                  /*tag=c
XX
PN
    EP293785-A.
XX
PD
    07-DEC-1988.
XX
PF
                 88EP-0108528.
    27-MAY-1988;
XX
PR
    29-MAY-1987;
                 87US-0055662.
                 88US-0147842.
PR
    25-JAN-1988;
XX
    (ONCO ) ONCOGEN.
PA
    (BRIM ) BRISTOL-MYERS CO.
PA
XX
ΡI
    Purchio AG, Gentry L, Twardzik D;
XX
    WPI; 1988-347488/49.
DR
    P-PSDB; AAP80647.
DR
XX
    Prodn. of simian transforming growth factor beta-1 - by culturing
PT
    transfected eucaryotic cells, and new precursor proteins, useful for
PT
PT
    treating tumours.
XX
PS
    Disclosure; Page ?; pp; English.
XX
    The cDNA is prepd. from African green monkey cell line BSC-40 and is
CC
    expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC
    between mature simian and human TGF-beta 1. The plasmid also contains
CC
    the SV40 promoter and a selection marker, esp. DHFR.
CC
CC
    (Updated on 25-MAR-2003 to correct PA field.)
CC
    (Updated on 25-MAR-2003 to correct PI field.)
XX
    Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
SO
                       79.6%; Score 953.4; DB 9; Length 1560;
 Query Match
                       88.3%; Pred. No. 1.6e-192;
 Best Local Similarity
 Matches 1057; Conservative 0; Mismatches 116; Indels
                                                        24; Gaps
           Qу
            Db
```

Qy	61	CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	120
Db	321		380
Qу	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	381	GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	440
Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	500
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGGGGGGGGG	560
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	561	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	620
Qy	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	621	TATGACAAGTTCAAGCAGAGCACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	681	CGAGAAGCAGTACCTGAACCTGTTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	740
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	741	AAGTTAAAAGTCGAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	800
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	801	TACCTCAGCAACCGGCTGCTGGCGCCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	860
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	861	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	920
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	921	GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	981	ACCGGCCGCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1040
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1041	ATGCCACCCCCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA	1094
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1095		1136
Qу	901	$\tt TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT$	960

```
1137 TGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1196
Db
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
QУ
            1197 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG 1256
Db
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
QУ
            1257 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1316
Db
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
QУ
            1317 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1376
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
            1377 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
Dh
RESULT 13
AA003508
    AAO03508 standard; DNA; 1560 BP.
XX
AC
    AAQ03508;
XX
    25-MAR-2003 (updated)
DT
    09-JAN-2003 (updated)
DT
    14-AUG-1990 (first entry)
DT
XX
DE
    Simian Transforming growth factor - Betal.
XX
    HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW
    factors; ds.
KW
XX
    Cebus apella.
OS
XX
                 Location/Qualifiers
FΗ
    Key
                 267..1437
FT
    CDS
                  /*taq=a
FT
    mat peptide
                 1103..1437
FT
FT
                  /*tag=b
XX
PN
    EP356935-A.
XX
    07-MAR-1990.
PD
XX
PF
    25-AUG-1989; 89EP-0115719.
XX
PR
    25-AUG-1988; 88US-0236698.
XX
    (ONCO ) ONCOGEN LP.
PΑ
XX
    Brankovan V, Lioubin M, Purchio A;
PΙ
XX
    WPI; 1990-068723/10.
DR
    P-PSDB; AAR05663.
DR
```

```
XX
PT
   Compsns. contg. transforming growth factor beta -
PT
   used for inhibitions of HIV infection and replication in vivo.
XX
PS
   Disclosure; Fig 1; 20pp; English.
ХX
CC
   TGF-beta may be used in vivo to prevent formation of synctia and
   inhibit HIV infection. TGF may also be used with other HIV treatments
CC
CC
   (AZT, soluble CD4 etc.).
   (Updated on 09-JAN-2003 to add missing OS field.)
CC
   (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
 Query Match
                   79.6%; Score 953.4; DB 11; Length 1560;
                  88.3%; Pred. No. 1.6e-192;
 Best Local Similarity
                        0; Mismatches 116; Indels
 Matches 1057; Conservative
                                              24; Gaps
                                                        1;
        Qу
          Db
        61 CTGACGCCTGGCCGGCCGCCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          321 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG 380
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          381 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 440
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          441 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 500
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          501 TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGAGTGCGGAGCCCGAACCGGAG 560
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
          561 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 620
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          621 TATGACAAGTTCAAGCAGAGCACACAGCATATATATGTTCTTCAACACATCAGAGCTC 680
Db
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
          Db
       681 CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 740
       481 AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
          741 AAGTTAAAAGTCGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 800
Db
       541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Qу
          801 TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC 860
Db
```

```
601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT 660
Qу
          861 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 920
Db
       661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qу
          921 GCCCACTGCTCCTGTGACAGCAAAGATAACACTGCAAGTGGACATCAACGGGTTCACT 980
Db
       721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
           Db
       981 ACCGGCCGCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1040
       781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
          Db
      1041 ATGGCCACCCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA----- 1094
       841 AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                        Db
      1095 ------GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 1136
       901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
QУ
          1137 TGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1196
Dh
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
          1197 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTG 1256
Db
      1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCG 1080
Qу
          1257 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1316
Db
      1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGACTACGTGGGCCGC 1140
Qу
          1317 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1376
Db
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
QУ
          1377 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
Db
RESULT 14
AAV52933
   AAV52933 standard; cDNA; 2537 BP.
ID
XX
AC
   AAV52933;
XX
DT
   25-MAR-2003
             (updated)
DT
   21-DEC-1998
             (first entry)
XX
DE
   Human pre-transforming growth factor-beta 1 cDNA.
XX
   Transforming growth factor-beta 1; TGF-beta 1; human; ss.
KW
XX
```

OS

XX

Homo sapiens.

```
FH
     Key
                     Location/Qualifiers
FT
     CDS
                     842..2014
FT
                     /*tag=a
FT
     mat peptide
                     1676..2011
FT
                     /*taq=b
FT
     stem loop
                     37..113
FT
                     /*tag=b
                     /note= "putative stable hairpin loop"
FT
FT
     misc feature
                     2015..2100
FT
                     /*tag= c
FT
                     /note= "GC-rich sequence"
FT
     polyA signal
                     2514..2520
FT
                     /*tag= d
XX
PN
     US5801231-A.
XX
PD
     01-SEP-1998.
XX
PF
     30-MAY-1995;
                    95US-0454468.
XX
PR
     13-MAR-1987;
                    87US-0025423.
PR
     22-MAR-1985;
                    85US-0715142.
                    89US-0389929.
PR
     04-AUG-1989;
PR
     04-MAR-1992;
                   92US-0845893.
     05-NOV-1993;
PR
                   93US-0147364.
PR
     30-MAY-1995;
                    95US-0454468.
XX
PA
     (GETH ) GENENTECH INC.
XX
PΙ
     Derynck RMA, Goeddel DV;
XX
     WPI; 1998-494840/42.
DR
DR
     P-PSDB; AAW78785.
XX
     DNA encoding transforming growth factor-beta precursor sequence -
PΤ
PT
     useful for analysis to perform manipulations to increase yield of
PT
     recombinant production of the protein
XX
     Example 3; Fig 1B 1-3; 26pp; English.
PS
XX
CC
     This nucleotide sequence codes for the human transforming growth
     factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC
CC
     composite of overlapping cDNA clones isolated from different cDNA
     libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC
CC
     TGF-beta exon (see AAV52936) restriction fragments as probes.
CC
     The 3' region of the sequence was determined using cloned genomic
CC
          The invention relates to the recombinant production of
CC
     TGF-beta. Biologically active TGF-beta is defined as being capable
CC
     of inducing EGF-potentiated anchorage independent growth of target
CC
     cell lines and/or growth inhibition of neoplastic cell lines.
CC
     Nucleic acids encoding TGF-beta have been isolated and cloned into
CC
     vectors which are replicated in bacteria and expressed in
CC
     eukaryotic cells. TGF-beta recovered from transformed cells is
CC
     used in known therapeutic applications. TGF-beta nucleic acids are
CC
     also useful in diagnosis and identification of TGF-beta clones.
CC
     (Updated on 25-MAR-2003 to correct PF field.)
XX
```

79.5%; Score 951.8; DB 19; Length 2537; Query Match 88.2%; Pred. No. 3.6e-192; Best Local Similarity Matches 1056; Conservative 0; Mismatches 117; Indels 24; Gaps 1; Qу Db 61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120 Qу Db 902 CTGACGCCTGGCCCGCCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCAG 961 121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180 Qу 962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021 Db 181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240 QУ 1022 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGTGCCCGAGGCCGTGCTCGCCCTG 1081 Db 241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300 Qу 1082 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 1141 Db 301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360 Qу 1142 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 1201 Db 361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420 Qу 1202 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 1261 Db 421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480 Qу 1262 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 1321 Db 481 AAGTTAAAAGTGGAGCACCTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540 Qу 1322 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1381 Db 541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600 Qy 1382 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1441 Db 601 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660 Qу 1442 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGAGAAATTGAGGGCTTTCGCCTTAGC 1501 Db 661 GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720 Qу 1502 GCCCACTGCTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 1561 Db 721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780 Qу 1562 ACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1621 Db

```
781 ATGGCCACCCGGTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Qу
           1622 ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA----- 1675
Db
        841 AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Qу
                          --GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1717
Db
        901 TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Qу
           1718 TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1777
Db
        961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Qу
           Db
       1778 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1837
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
           1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
Db
       1081 \ \ GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC \ \ 1140
Qу
           1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Db
RESULT 15
ABV75391
    ABV75391 standard; DNA; 1176 BP.
ID
XX
AC
    ABV75391;
XX
DT
    18-MAR-2003 (first entry)
XX
    TGFB1 Arg25Pro polymorphism G-allele nucleotide sequence.
DE
XX
    Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;
KW
    renal failure; nephrotropic; human; gene; ds.
KW
XX
OS
    Homo sapiens.
XX
                 Location/Qualifiers
FΗ
    Key
                 1..1176
FT
    CDS
                 /*tag= a
FT
XX
    WO200290585-A2.
PN
XX
PD
    14-NOV-2002.
XX
    08-MAY-2002; 2002WO-GB02066.
PF
ХX
    09-MAY-2001; 2001GB-0011277.
PR
XX
```

```
(UYSH-) UNIV SHEFFIELD HALLAM.
PA
XX
ΡI
    El-Nahas AM, Blakemore A, Khalil MS;
XX
DR
    WPI; 2003-120560/11.
    P-PSDB; ABB82780.
DR
XX
PT
    Determining an individual's susceptibility to the progression of renal
PT
    failure comprises detecting the presence of a genetic polymorphism
    pattern in transforming growth factor beta 1 (TGFB1) gene in a sample
PT
PT
    from the individual -
XX
PS
    Claim 49; Page 58; 62pp; English.
XX
CC
    The invention relates to determining an individual's susceptibility to
    renal failure and invovles detecting the presence of a genetic
CC
CC
    polymorphism pattern in transforming growth factor beta 1 (TGFB1) gene in
CC
    a sample from an individual, where polymorphism pattern is associated
    with renal failure. The method is useful for determining an individual's
CC
    susceptibility to the progression of renal failure. The nucleic acid
CC
CC
    comprising a T(-509)C polymorphism of TGFB1 gene, or a polypeptide
CC
    comprising a sequence of 391 amino acids is useful for preparing a
CC
    medicament for retarding or preventing the progression of renal disease,
CC
    and for drug research purposes for retarding or preventing the
CC
    progression of renal disease. Sequences ABV75386-88 represents the
    nucleotide sequence for the TGFB1 G-allele of the Arg25Pro polymorphism
CC
CC
    of exon 1.
XX
SO
    Sequence 1176 BP; 239 A; 381 C; 354 G; 202 T; 0 other;
                     79.0%; Score 945.2; DB 25; Length 1176;
                     88.3%; Pred. No. 8.1e-191;
 Best Local Similarity
 Matches 1060; Conservative 0; Mismatches 113; Indels
                                                    27; Gaps
                                                              2;
Qу
          Db
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           61 CTGACGCCTGGCCGGCCGCCGCGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 120
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
        Db
        181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
QУ
           Db
        181 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGGTGCCCGAGGCCGTGCTCGCCCTG 240
        241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
           241 TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGACCGGAGCCCGAGCCTGAG 300
Db
        301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
           301 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 360
Dh
```

QУ	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	361		420
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGG	477
Db	421	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGG	480
Qy	478	CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG	537
Db	481	CTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG	540
Qy	538	CGCTACCTCAGCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT	597
Db	541		600
Qy	598	GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC	657
Db	601		660
Qy	658	AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC	717
Db	661	AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC	720
Qу	718	AATTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	777
Db	721	ACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT	780
Qy	778	CTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	781		837
Qy	838	TACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
Db	838		876
Qy	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
Db	877		936
Qy	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1017
Db	937	CACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGC	996
Qy	1018	CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG	1077
Db	997		1056
Qy	1078	GCGGCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC	1137
Db	1057		1116
Qy	1138	CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA	1197
Dh	1117		1176

Search completed: October 27, 2003, 19:10:53

Job time : 373.617 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 18:35:27; Search time 355.784 Seconds

(without alignments)

9022.658 Million cell updates/sec

Title: US-10-017-372E-8

Perfect score: 1197

Sequence: 1 atggcgccttcggggctgcg.....gttcctgcaagtgcagctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 segs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cqn2 6/ptodata/2/pubpna/PCTUS PUBCOMB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2 6/ptodata/2/pubpna/US09B PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*

13: /cgn2 6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

14: /cgn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10 NEW PUB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res			Query				
	No.	Score	Match	Length	DB	ID	Description
	1	958.2	80.1	1821	14	US-10-087-268-1	Sequence 1, Appli
	2	958.2	80.1	2742	14	US-10-037-270-220	Sequence 220, App
	3	956.6	79.9	1821	14	US-10-087-268-4	Sequence 4, Appli
	4	943.6	78.8	2745	11	US-09-948-002-28	Sequence 28, Appl
	5	854.2	71.4	1585	11	US-09-948-002-27	Sequence 27, Appl
	6	847.8	70.8	2094	11	US-09-948-002-1	Sequence 1, Appli
	7	654	54.6	1376	10	US-09-756-283A-19	Sequence 19, Appl
	8	591.4	49.4	1352	10	US-09-756-283A-21	Sequence 21, Appl
	9	344	28.7	489	11	US-09-911-904-167	Sequence 167, App
	10	308.6	25.8	339	10	US-09-813-271B-1	Sequence 1, Appli
	11	227.2	19.0	336	10	US-09-813-271B-7	Sequence 7, Appli
	12	225.6	18.8	4382	12	US-09-957-458B-9	Sequence 9, Appli
	13	224.4	18.7	2574	11	US-09-906-158-3	Sequence 3, Appli
	14	224.4	18.7	2574	13	US-10-028-158-20	Sequence 20, Appl
	15	220.4	18.4	2879	11	US-09-906-158-10	Sequence 10, Appl
	16	209.4	17.5	339	10	US-09-813-271B-5	Sequence 5, Appli
С	17	185.2	15.5	2381	12	US-10-311-455-2384	Sequence 2384, Ap
	18	182.4	15.2	336	10	US-09-813-271B-11	Sequence 11, Appl
	19	181.2	15.1	2381	12	US-10-311-455-2383	Sequence 2383, Ap
	20	180.8	15.1	336	10	US-09-813-271B-9	Sequence 9, Appli
	21	166.2	13.9	4267	11	US-09-948-002-47	Sequence 47, Appl
	22	158.2	13.2	339	10	US-09-813-271B-3	Sequence 3, Appli
	23	158.2	13.2	2570	12	US-09-960-706-663	Sequence 663, App
	24	158.2	13.2	2912	13	US-10-044-090-323	Sequence 323, App
С	25	141.6	11.8	597	9	US-09-864-761-15319	Sequence 15319, A
С	26	134.8	11.3	154	9	US-09-864-761-31841	Sequence 31841, A
C	27	131.8	11.0	206	10	US-09-833-381-577	Sequence 577, App
	28	113.8	9.5	181	10	US-09-833-381-1416	Sequence 1416, Ap
C	29	110	9.2	537	9	US-09-864-761-8844	Sequence 8844, Ap
С	30	109	9.1	148	9	US-09-864-761-25510	Sequence 25510, A
	31	104.8	8.8	851 29000	13 11	US-10-027-632-152938 US-09-906-158-17	Sequence 152938, Sequence 17, Appl
	32 33	101.6 100.4	8.5 8.4	29000	10	US-09-833-381-73	Sequence 73, Appl
С	34	73.2	6.1	450	11	US-09-918-995-6145	Sequence 6145, Ap
С	35	69.8	5.8	431	9	US-09-864-761-18644	Sequence 18644, A
c	36	69.4	5.8	176	10	US-09-833-381-571	Sequence 571, App
_	37	69				US-10-029-386-9758	Sequence 9758, Ap
	38	68.2	5.7	176	12	US-10-029-386-23458	Sequence 23458, A
С	39	64	5.3	363	10	US-09-833-381-585	Sequence 585, App
_	40	62.6	5.2	364	12	US-10-029-386-26476	Sequence 26476, A
	41	62.6	5.2	544	12	US-10-029-386-12776	Sequence 12776, A
	42	62.6	5.2	927	12	US-10-244-718-1	Sequence 1, Appli
	43	57.4	4.8	486	11	US-09-918-995-25641	Sequence 25641, A
	44	55.2	4.6	594	13	US-10-027-632-141376	Sequence 141376,
	45	52	4.3	1004	8	US-08-957-425-10	Sequence 10, Appl
			_				•

ALIGNMENTS

RESULT 1 US-10-087-268-1

[;] Sequence 1, Application US/10087268 ; Publication No. US20030119010A1

```
; GENERAL INFORMATION:
  APPLICANT: Jonsonn, Julie Ruth
  APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
  FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEO ID NO 1
  LENGTH: 1821
   TYPE: DNA
  ORGANISM: Human
   FEATURE:
  NAME/KEY: 5'UTR
  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
  OTHER INFORMATION:
  NAME/KEY: sig peptide
  LOCATION: (512)..(598)
  OTHER INFORMATION:
  NAME/KEY: 3'UTR
   LOCATION: (1685)..(1821)
  OTHER INFORMATION:
US-10-087-268-1
 Query Match
                   80.1%; Score 958.2; DB 14; Length 1821;
 Best Local Similarity
                  88.6%; Pred. No. 1.2e-258;
 Matches 1060; Conservative
                        0; Mismatches 113; Indels
                                                24; Gaps
                                                          1;
         Qу
          Db
       61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
QУ
          572 CTGACGCCTGGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 631
Db
Qу
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
          Db
       632 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 691
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qy
          Db
       692 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 751
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          752 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGACTGCAGAACCGGAGCCCGAGCCTGAG 811
Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
          812 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 871
Db
```

Qy	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Db	872	
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Db	932	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 991
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Db	992	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 1051
Qy	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
Db	1052	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 1111
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
Db	1112	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGGCTTTCGCCTTAGC 1171
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720
Db	1172	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 1231
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Db	1232	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1291
Qy	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC 840
Db	1292	ATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA 1345
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC 900
Db	1346	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAAC 1387
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT 960
Db	1388	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC 1447
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
Db	1448	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1507
Qу	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Db	1508	GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1567
Qу	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
Db	1568	GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1627
Qy	1141	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Db	1628	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1684

```
RESULT 2
US-10-037-270-220
; Sequence 220, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
  APPLICANT: Liu, Chenghua
  APPLICANT: Asundi, Vinod
  APPLICANT: Zhang, Jie
  APPLICANT: Ren, Feiyan
  APPLICANT: Chen, Rui-hong
  APPLICANT: Zhao, Qing A.
  APPLICANT: Wehrman, Tom
  APPLICANT: Xue, Aidong J.
  APPLICANT: Yang, Yonghong APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yunqing
  APPLICANT: Wang, Dunrui
  APPLICANT: Wang, Zhiwei
  APPLICANT: Tillinghast, John
  APPLICANT: Drmanac, Radoje T.
  TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
  TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/10/037,270
 CURRENT FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 09/552,317
  PRIOR FILING DATE: 2000-04-25
  PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1104
  SOFTWARE: pt FL genes Version 1.0
; SEO ID NO 220
  LENGTH: 2742
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (842)..(2014)
US-10-037-270-220
 Query Match
                     80.1%; Score 958.2; DB 14; Length 2742;
 Best Local Similarity 88.6%; Pred. No. 1.3e-258;
 Matches 1060; Conservative 0; Mismatches 113; Indels 24; Gaps
                                                                1;
QУ
          Db
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           Db
        902 CTGACGCCTGGCCGGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
QУ
           Dh
        962 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 1021
```

Qy	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	1022	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCTG	1081
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	1141
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qy	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACACAGCATATATAT	1261
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1262	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	1321
Qy	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1322	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1381
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1382	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1441
Qy	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1442	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1501
Qy	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1502	GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT	1561
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1562	ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1621
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1622	ATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1675
Qy	841	AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1676		1717
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1718	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1777
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
da	1778	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG	1837

```
1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
Qу
           Db
      1838 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCG 1897
      1081 GCGCCGTGCTGCGCGCGCGCGCGCGCCCATCGTGTACTACGTGGCCGC 1140
Qу
           1898 GCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1957
Db
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           1958 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
Db
RESULT 3
US-10-087-268-4
; Sequence 4, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
 CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
  LENGTH: 1821
   TYPE: DNA
  ORGANISM: Human
  FEATURE:
  NAME/KEY: 5'UTR
  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
  OTHER INFORMATION:
  NAME/KEY: sig peptide
  LOCATION: (512)..(598)
   OTHER INFORMATION:
   NAME/KEY: 3'UTR
  LOCATION: (1685)..(1821)
   OTHER INFORMATION:
US-10-087-268-4
 Query Match
                    79.9%; Score 956.6; DB 14; Length 1821;
 Best Local Similarity 88.5%; Pred. No. 3.3e-258;
 Matches 1059; Conservative
                         0; Mismatches 114; Indels
                                                 24; Gaps
                                                           1;
Qу
         Db
       61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
           Db
       572 CTGACGCCTGGCCGGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 631
```

Qу	121	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	180
Db	632	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	691
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	692	AGCCCCCGAGCCAGGGGGAGGTGCCCCCGGCCCGGCCCG	751
Qy	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	752	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCTGAG	811
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	812	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	871
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	872	TATGACAAGTTCAAGCAGAGTACACACACACATCATATATTCTTCTTCAACACATCAGAGCTC	931
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	932	CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	991
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	992	AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	1051
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1052	TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC	1111
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1112	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	1171
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1172		1231
Qy	721	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1232	ACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1291
Qу	781	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1292	ATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1345
Qу	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1346		1387
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1388	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	1447

```
Qу
       961 GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA 1020
          Db
       1448 GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTG 1507
Qу
       1021 GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG 1080
          Db
      1508 GACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCG 1567
Qу
       1081 GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
          Db
       1568 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC 1627
Qу
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
           Db
      1628 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1684
RESULT 4
US-09-948-002-28
; Sequence 28, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                           EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
 SEO ID NO 28
   LENGTH: 2745
  TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
  NAME/KEY: CDS
   LOCATION: (842)...(2017)
US-09-948-002-28
 Query Match
                   78.8%; Score 943.6; DB 11; Length 2745;
 Best Local Similarity 88.2%; Pred. No. 1.7e-254;
 Matches 1059; Conservative 0; Mismatches 114; Indels
                                               27; Gaps
                                                         2;
         Qу
          Db
       Qу
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
          Db
       902 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 961
Qу
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
```

Db	962	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	1021
Qу	181	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	240
Db	1022	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGAGGCCGTGCTCGCCCTG	1081
Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1082	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG	1141
Qу	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1142	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	1201
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1202	TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	1261
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGG	477
Db	1262		1321
Qу	478	CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG	537
Db	1322	CTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG	1381
Qу	538	CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT	597
Db	1382		1441
Qу	598	GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC	657
Db	1442	GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT	1501
Qу	658	AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC	717
Db	1502		1561
Qу	718	AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	777
Db	1562	ACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT	1621
Qу	778	CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	1622	CTCATGGCCACCCGGTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	1678
Qу	838	TACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
ДЪ	1679	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAG	1717
Qу	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
Db	1718	AACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATC	1777
Qу	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1017
Db	1778	CACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGC	1837

```
1018 CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG 1077
Qу
           1838 CTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCG 1897
Db
       1078 GCGGCGCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC 1137
Qу
           Db
       1898 GCGGCGCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGC 1957
       1138 CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           Db
       1958 CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2017
RESULT 5
US-09-948-002-27
; Sequence 27, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                             EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
 SEQ ID NO 27
   LENGTH: 1585
   TYPE: DNA
   ORGANISM: Rattus norvegicus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (413)...(1585)
US-09-948-002-27
                    71.4%; Score 854.2; DB 11; Length 1585;
 Query Match
 Best Local Similarity 83.1%; Pred. No. 1.7e-229;
 Matches 995; Conservative 0; Mismatches 178; Indels
                                                  24; Gaps
                                                             1:
         QУ
           Db
        413 ATGCCGCCTCGGGGCTGCGGCTGCTGCTCTCCCACTCCCGTGGCTTCTAGTG 472
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
QУ
           473 CTGACGCCCGGGAGGCCAGCCGCGGGACTCTCCACCTGCAAGACCATCGACATGGAGCTG 532
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           Db
        533 GTGAAACGGAAGCGATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGCTCGCC 592
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
QУ
```

Db	593	AGTCCCCGAGCCAGGGGAGGTACCGCCGGGCCCGCTGCCCGAGGCGGTGCTCGCTTTG	652
Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	653	TACAACAGCACCCGCGACCGGGTGGCAGGCGAGAGCCCGAGCCCGAG	712
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	713	GCGGACTACTACGCCAAAGAAGTCACCCGCGTGCTAATGGTGGACCGCAACAACGCAATC	772
Qy	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	773	TATGACAAAACCAAAGACATCACACACAGTATATATATGTTCTTCAATACGTCAGACATT	832
Qγ	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db		CGGGAAGCAGTGCCAGAACCCCCATTGCTGTCCCGTGCAGAGCTGCGCCTGCAGAGATTC	
Qу		AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	
Db		AAGTCAACTGTGGAGCAACACGTAGAACTCTACCAGAAATATAGCAACAATTCCTGGCGT	
Qу		TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	
Db		TACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCCTGAGTGGCTGTCTTTTGACGTC	
Qy 21		ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	
Db		ACTGGAGTTGTCCGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGCTTCAGT	
Qy Db		GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	
			780
Qy Db			
Qу		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	
Db		ATGGCCACCCCCTGGAAAGGGCTCAACACCTGCACAGCTCCAGGCACCGGAGA	
Qy		AAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	
Db			
Qу	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1289		1348
Qу	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1349	GAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGGCCCTGCCCCTACATTTGGAGCCTG	1408
Qу	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080

```
Db
       Qу
       1081 GCGCCGTGCTGCGCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1140
           Db
       1469 TCACCGTGCTGCGCGCAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGC 1528
Qу
       1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
           Db
       1529 AAGCCCAAGGTGGAGCAGTTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1585
RESULT 6
US-09-948-002-1
; Sequence 1, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
 APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                           EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
 NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 1
  LENGTH: 2094
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: CDS
  LOCATION: (868)...(2040)
US-09-948-002-1
 Query Match
                   70.8%; Score 847.8; DB 11; Length 2094;
 Best Local Similarity 82.8%; Pred. No. 1.2e-227;
 Matches 991; Conservative 0; Mismatches 182; Indels
                                                          1:
Qу
         868 ATGCCGCCTCGGGGCTGCGGCTACTGCCGCTTCTGCTCCCACTCCCGTGGCTTCTAGTG 927
Db
Qу
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
           Db
       928 CTGACGCCCGGGAGGCCAGCCGCGGGACTCTCCACCTGCAAGACCATCGACATGGAGCTG 987
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
           Db
       988 GTGAAACGGAAGCGCATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGCTCGCC 1047
Qу
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
          Db
       1048 AGTCCCCCAAGCCAGGGGGAGGTACCGCCCGGCCCGCTGCCCGAGGCGGTGCTCGCTTTG 1107
```

Qу	241	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	300
Db	1108		1167
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	1168	GCGGACTACTATGCTAAAGAGGTCACCCGCGTGCTAATGGTGGACCGCAACAACGCCATC	1227
Qу	361	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	1228	TATGAGAAAACCAAAGACATCTCACACAGTATATATATGTTCTTCAATACGTCAGACATT	1287
Qу	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	1288	CGGGAAGCAGTGCCCGAACCCCCATTGCTGTCCCGTGCAGAGCTGCGCTTGCAGAGATTA	1347
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	540
Db	1348	AAATCAAGTGTGGAGCAACATGTGGAACTCTACCAGAAATATAGCAACAATTCCTGGCGT	1407
Qу	541	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	600
Db	1408	TACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCCTGAGTGGCTGTCTTTTGACGTC	1467
Qу	601	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	660
Db	1468	ACTGGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGATTCAGC	1527
Qу	661	GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	720
Db	1528	GCTCACTGCTCTTGTGACAGCAAAGATAACAAACTCCACGTGGAAATCAACGGGATCAGC	1587
Qy	721	TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	780
Db	1588	CCCAAACGTCGGGGCGACCTGGGCACCATCCATGACATGAACCGGCCCTTCCTGCTCCTC	1647
Qy	781	ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTAC	840
Db	1648	ATGGCCACCCCCTGGAAAGGGCCCAGCACCTGCACAGCTCACGGCACCGGAGA	1701
Qy	841	AAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	900
Db	1702	GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGAAC	1743
Qy	901	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCAT	960
Db	1744	TGCTGTGTGCGGCAGCTGTACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCAC	1803
Qy	961	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1020
Db	1804	GAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGACCCTGCCCCTATATTTGGAGCCTG	1863
QУ	1021	GACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCG	1080
Db	1864	GACACACAGTACAGCAAGGTCCTTGCCCTCTACAACCAAC	1923
QУ	1081	GCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1140

```
Db
      1924 TCACCGTGCTGCGCGCAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGC 1983
      1141 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
      1984 AAGCCCAAGGTGGAGCAGTTGTCCAACATGATTGTGCGCTCCTGCAAGTGCAGCTGA 2040
RESULT 7
US-09-756-283A-19
; Sequence 19, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
 APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
 FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEO ID NO 19
  LENGTH: 1376
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: LAP-mIFNbeta construct
   NAME/KEY: CDS
   LOCATION: (1)..(1368)
US-09-756-283A-19
 Query Match
                   54.6%; Score 654; DB 10; Length 1376;
 Best Local Similarity
                   88.1%; Pred. No. 2.4e-173;
 Matches 724; Conservative
                       0; Mismatches 95; Indels
                                                 3; Gaps
                                                          1:
         Qу
          Db
        61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
          61 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 120
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
QУ
          Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 180
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          181 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 240
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          241 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGATGCAGAACCGGAGCCCGAGCCTGAG 300
Db
0v
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
```

```
Db
       301 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 360
       361 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          Db
       361 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 420
Qу
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT---GAGG 477
          421 CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCCGGGCAGAGCTGCGTCTGCTGAGGAGG 480
Db
QУ
       478 CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG 537
          Db
       481 CTCAAGTTAAAAGTGGAGCACCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG 540
       538 CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT 597
Qу
          541 CGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGAT 600
Db
       598 GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC 657
Qу
          601 GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT 660
Db
       658 AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC 717
Qу
          661 AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC 720
Db
       718 AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC 777
Qу
          721 ACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT 780
Dh
       778 CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGC 819
Qу
          Db
       781 CTCATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGC 822
```

```
RESULT 8
US-09-756-283A-21
; Sequence 21, Application US/09756283A
; Patent No. US20020151478A1
 GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
   LENGTH: 1352
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: mIFNbeta-LAP construct
```

NAME/KEY: CDS

; LOCATION: (1)..(1344) US-09-756-283A-21

	cal .	49.4%; Score 591.4; DB 10; Length 1352; Similarity 87.0%; Pred. No. 8.6e-156; 2; Conservative 0; Mismatches 96; Indels 3; Gaps	1;
Qy	63	GACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTGGT	122
Db	582	GGCGGAGGGGCTCAGCGGCCGCACTATCCACCTGCAAGACTATCGACATGGAGCTGGT	641
Qy	123	GAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAG	182
Db	642	GAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAG	701
Qy	183	CCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTA	242
Db	702	CCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTGTA	761
Qу	243	CAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGC	302
Db	762	CAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGC	821
Qy	303	GGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTA	362
Db	822	CGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTA	881
Qy	363		422
Db	882	TGACAAGTTCAAGCAGAGTACACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCG	941
Qy	423	GGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCT	479
Db	942	AGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGGCT	1001
Qу	480	CAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCG	539
Db	1002	CAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCG	1061
Qу	540	CTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGT	599
Db	1062	ATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGT	1121
Qу	600	CACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAG	659
Db	1122	CACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAG	1181
Qy	660	TGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAA	719
Db	1182	CGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCAC	1241
Qy	720	TTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCT	779
Db	1242	TACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCT	1301
Qу	780	CATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCT 820	

```
RESULT 9
US-09-911-904-167
; Sequence 167, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
 APPLICANT: Farr, Spencer B.
 APPLICANT: Pickett, Gavin G.
 APPLICANT: Neft, Robin Eileen
 APPLICANT: Dunn, II, Robert Thomas
  TITLE OF INVENTION: CANINE TOXICITY GENES
  FILE REFERENCE: 400742000200
  CURRENT APPLICATION NUMBER: US/09/911,904
  CURRENT FILING DATE: 2002-04-09
  PRIOR APPLICATION NUMBER: US 60/220,057
 PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEO ID NOS: 386
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
   LENGTH: 489
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: misc feature
   LOCATION: (1)...(489)
   OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167
 Query Match
                     28.7%; Score 344; DB 11; Length 489;
 Best Local Similarity 89.9%; Pred. No. 1.6e-86;
 Matches 390; Conservative 0; Mismatches 20; Indels 24; Gaps
        764 GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCC 823
Qу
           1 GACCCTTCCTGCTCCTCATGGCCACCCCACTGGAGAGGGCCCAGCACCTGCACAGCTCCC 60
Db
        824 GGCACCGCGAGACTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCA 883
Qу
           61 GGCAGCGCCG-------GGCCCTGGACACCAACTACTGCTTCA 96
Db
        884 GCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGG 943
Qу
           97 GCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCTCTACATTGACTTCCGCAAGGATCTGG 156
Db
        944 GCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTC 1003
Qу
           Db
        157 GCTGGAAGTGGATCCATGAGCCCAAGGGTTACCACGCTAACTTCTGCCTGGGGCCCTGCC 216
       1004 CCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACA 1063
Qу
           Db
        217 CCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCACA 276
       1064 ACCCGGGCGCGCGCGCGCCCTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCG 1123
Qу
           Db
        277 ACCCGGGCGCGCGCGCGCGCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCG 336
```

```
Qу
        1124 TGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCT 1183
             Db
         337 TGTACTACGTGGGCCGCAAGCCCAAGCTGGAGCAGCTGTCGAACATGATCGTGCGCTCCT 396
        1184 GCAAGTGCAGCTGA 1197
QУ
              Db
         397 GCAAGTGCAGCTGA 410
RESULT 10
US-09-813-271B-1
; Sequence 1, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
        APPLICANT:
                    (A) Nico Cerletti
        TITLE OF INVENTION: New process for the production of
                            biologically active protein
        NUMBER OF SEQUENCES: 13
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: No. US20020115834Alartis Patent Department
             STREET: 564 Morris Avenue
             CITY: Summit
             STATE: New Jersey
             COUNTRY: USA
             ZIP: 07901
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/813,271B
             FILING DATE: 20-Mar-2001
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: PCT/EP95/02719
             FILING DATE: 12-Jul-95
             APPLICATION NUMBER: EPO 94810439.3
             FILING DATE: 25-Jul-94
        ATTORNEY/AGENT INFORMATION:
             NAME: Pfeiffer, Hesna J. .
             REGISTRATION NUMBER: 22640
             REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (908) 522-6940
             TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 1:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 339 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA to mRNA
        HYPOTHETICAL: NO
        IMMEDIATE SOURCE:
             CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
```

```
FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "human TGF-betal"
       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1
 Query Match
                    25.8%; Score 308.6; DB 10; Length 339;
 Best Local Similarity
                   94.4%; Pred. No. 1.3e-76;
 Matches 320; Conservative
                         0; Mismatches
                                     19; Indels
                                                 0; Gaps
                                                           0;
Qу
       Db
         919 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 978
Qу
          Db
        61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
       979 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1038
Qу
           Db
       121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Qу
      1039 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCG 1098
           181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGGCGC 240
Db
       1099 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1158
Qу
           Db
       241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
      1159 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
          Db
       301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 11
US-09-813-271B-7
; Sequence 7, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
      APPLICANT:
               (A) Nico Cerletti
      TITLE OF INVENTION: New process for the production of
                      biologically active protein
      NUMBER OF SEQUENCES: 13
      CORRESPONDENCE ADDRESS:
          ADDRESSEE: No. US20020115834Alartis Patent Department
          STREET: 564 Morris Avenue
          CITY: Summit
          STATE: New Jersey
          COUNTRY: USA
          ZIP: 07901
      COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/813.271B
            FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: PCT/EP95/02719
            FILING DATE: 12-Jul-95
            APPLICATION NUMBER: EPO 94810439.3
            FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
            NAME: Pfeiffer, Hesna J. .
            REGISTRATION NUMBER: 22640
            REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (908) 522-6940
            TELEFAX: (908) 522-6955
  INFORMATION FOR SEQ ID NO: 7:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 336 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
       MOLECULE TYPE: other nucleic acid
            DESCRIPTION: /desc = "recombinant hybrid DNA of
       IMMEDIATE SOURCE:
            CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
       FEATURE:
            NAME/KEY: mat peptide
            LOCATION: 1..132
            OTHER INFORMATION: /product= "N-terminal 44 amino
            acids of human TGF-betal"
       FEATURE:
            NAME/KEY: mat peptide
            LOCATION: 133..336
            OTHER INFORMATION: /product= "C-terminal 68 amino
            acids of human TGF-beta3"
       FEATURE:
            NAME/KEY: CDS
            LOCATION: 1..336
            OTHER INFORMATION: /product= "hybrid TGF-beta named
            TGF-beta1-3"
       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-813-271B-7
 Query Match
                      19.0%; Score 227.2; DB 10; Length 336;
 Best Local Similarity 79.8%; Pred. No. 8.6e-54;
 Matches 268; Conservative 0; Mismatches 68; Indels
                                                        0; Gaps
                                                                  0;
Qу
        Db
          919 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 978
Qу
            Db
         61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Qу
        979 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1038
```

```
Db
        121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACACCCACAGCACG 180
       Qу
           Db
        181 GTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCC 240
Qу
       1099 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1158
           Db
        241 CAGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 300
Qу
       1159 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGC 1194
           Db
        301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
RESULT 12
US-09-957-458B-9
; Sequence 9, Application US/09957458B
; Publication No. US20030166271A1
; GENERAL INFORMATION:
  APPLICANT: Chen, Una
  TITLE OF INVENTION: Method for growing stem cells
; FILE REFERENCE: P66567US0
 CURRENT APPLICATION NUMBER: US/09/957,458B
 CURRENT FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: PCT/EP00/08247
 PRIOR FILING DATE: 2000-08-24
  PRIOR APPLICATION NUMBER: EP 99116533
 PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
  LENGTH: 4382
  TYPE: DNA
  ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Vector for transforming supporting cell with a foreign to
express
   OTHER INFORMATION: a gene product of interest
US-09-957-458B-9
                    18.8%; Score 225.6; DB 12; Length 4382;
 Query Match
 Best Local Similarity 52.2%; Pred. No. 4.9e-53;
 Matches 652; Conservative 0; Mismatches 524; Indels 72; Gaps
                                                             4;
Qу
        16 CTGCGGCTCTTGCCGCTGCTGCCGCTGCTGTGGCTGCTGTGCTGACGCCTGGCCGG 75
           Db
        455 CTGCAGCCCATGCACTTGCAAAGGGCTCTGGTAGTCCTGGCCCTGCTGAACTTGGCCACA 514
        76 CCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGC 135
Qу
                    Db
        515 ATCAGCCTCTCTGTCCACTTGCACCACGTTGGACTTCGGCCACATCAAGAAGAAGAGG 574
Qу
        136 ATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCCGAGCCAG 195
            575 GTGGAAGCCATTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCA 634
```

Qy	196	GGGGACGTGCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGC	255
Db	635	TCGGTGATGACCCACGTCCCCTATCAGGTCCTGGCACTTTACAACAGCACCCGG	688
Qy	256	GACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCAGAG	300
Db	689	GAGTTGCTGGAAGAGATGCACGGGGAGAGGGAGGGAGGAGGCTGCACTCAGGAGACCTCGGAG	748
Qy	301	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	360
Db	749	TCTGAGTACTATGCCAAAGAGATCCATAAATTCGACATGATCCAGGGACTGGCGGAGCAC	808
Qу	361	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	420
Db	809	AATGAACTGGCCGTCTGCCCCAAAGGAATTACCTCTAAGGTTTTTCGTTTCAATGTGTCC	868
Qy	421	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	480
Db	869	TCAGTGGAGAAAATGGAACCAATCTGTTCCGGGCAGAGTTCCGGGTCTTGCGGGTGCCC	928
Qу	481	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAA	519
Db	929	AACCCCAGCTCCAAGCGCACAGAGCAGAGAATTGAGCTCTTCCAGATACTTCGACCGGAT	988
Qy	520	TACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCG	579
Db	989		1048
Qy	580	GAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCT	639
Db	1049	GAATGGCTGTCTTTCGATGTCACTGACACTGTGCGCGAGTGGCTGTTGAGGAGAGAGTCC	1108
Qy	640	ATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGC	681
Db	1109	AACTTGGGTCTGGAAATCAGCATCCACTGTCCATGTCACACCTTTCAGCCCAATGGAGAC	1168
Qy	682	AAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGC	729
Db	1169	ATACTGGAAAATGTTCATGAGGTGATGGAAATCAAATTCAAAGGAGTGGACAATGAAGAT	1228
Qy	730	CGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACC	789
Db	1229	GACCATGGCCGTGGAGACCTGGGGCGTCTCAAGAAGCAAAAGGATCACCACACCCACAC	1288
Qу	790	CCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCCGAGACTACAAGGATGAC	849
Db	1289	CTGATCCTCATGATGATCCCCCCACACCGACTGGACAGCCCAGGCCAGGCCAGGCAGTCAGAGG	1348
Qy	850	GACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTG	909
Db	1349	AAGAAGAGGCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGTA	1408
Qу	910	CGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAG	969
Db	1409	CGCCCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAG	1468

```
Qу
       970 GGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAG 1029
          Db
       1469 GGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGCGCAGACACACC 1528
      Qу
           Dh
      1529 CATAGCACGGTGCTTGGACTATACAACACCCTGAACCCAGAGGCGTCTGCCTCGCCATGC 1588
      1090 TGCGTGCCGCAGGCGCTGGAGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAG 1149
Qу
          Db
      1589 TGCGTCCCCCAGGACCTGGAGCCCCTGACCATCTTGTACTATGTGGGCAGAACCCCCAAG 1648
Qу
      1150 GTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
          Db
      1649 GTGGAGCAGCTGTCCAACATGGTGGTGAAGTCGTGTAAGTGCAGCTGA 1696
RESULT 13
US-09-906-158-3
; Sequence 3, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
 FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
 NUMBER OF SEQ ID NOS: 168
SEQ ID NO 3
  LENGTH: 2574
   TYPE: DNA
  ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (254)...(1492)
US-09-906-158-3
 Query Match
                   18.7%; Score 224.4; DB 11; Length 2574;
 Best Local Similarity 53.3%; Pred. No. 9.2e-53;
 Matches 660; Conservative 0; Mismatches 506; Indels
                                                72; Gaps
        Qу
              11 1
Db
       261 TGCACTTGCAAAGGGCTCTGGTGGTCCTGGCCCTGCTGAACTTTGCCACGGTCAGCCTCT 320
Qу
        86 GACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCA 145
            321 CTCTGTCCACTTGCACCACCTTGGACTTCGGCCACATCAAGAAGAAGAGGGTGGAAGCCA 380
Db
       146 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 205
Qу
          Db
       381 TTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCAACGGTGATGA 440
       206 CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG 265
Qу
```

Db	441	CCCACGTCCCCTATCAGGTCCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG 494
Qу	266	CCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGACTACT 310
Db	495	AGGAGATGCATGGGGAGGAGGGAAGGCTGCACCCAGGAAAACACCGAGTCGGAATACT 554
Qy	311	ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT 370
Db	555	ATGCCAAAGAAATCCATAAATTCGACATGATCCAGGGGCTGGCGGAGCACAACGAACTGG 614
Qy	371	TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG 430
Db	615	CTGTCTGCCCTAAAGGAATTACCTCCAAGGTTTTCCGCTTCAATGTGTCCTCAGTGGAGA 674
Qу	431	TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAG 490
Db	675	AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGGTGCCCAACCCCAGCT 734
QУ	491	TGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATG 529
Db	735	CTAAGCGGAATGAGCAGAGCACCTCTCCAGATCCTTCGGCCAGATGAGCACATTG 794
QУ	530	ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGT 589
Db	795	CCAAACAGCGCTATATCGGTGGCAAGAATCTGCCCACACGGGGCACTGCCGAGTGGCTGT 854
Qу	590	CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT 649
Db	855	CCTTTGATGTCACTGACACTGTGCGTGAGTGGCTGTTGAGAAGAGAGTCCAACTTAGGTC 914
Qу	650	TTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGG 703
Db	915	TAGAAATCAGCATTCACTGTCCATGTCACACCTTTCAGCCCAATGGAGATATCCTGGAAA 974
Qу	704	AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC 763
Db	975	ACATTCACGAGGTGATGGAAATCAAATTCAAAGGCGTGGACAATGAGGATGACCATGGCC 1034
Qy	764	GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGC 819
Db :	1035	GTGGAGATCTGGGGCCCTCAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCCTCA 1094
Qу	820	TCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGG 859
Db :	1095	TGATGATTCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGTCAGAGGAAGAAGCGGG 1154
Qу	860	CCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG
Db :	1155	CTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCTCT 1214
Qу	920	ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATG 979
Db :	1215	ACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTATG 1274
Qу	980	CCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGG 1039
Db 3	1275	CCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACAACCCACAGCACGG 1334

```
1040 TCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCCGC 1099
Qу
            Db
       1335 TGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCC 1394
       1100 AGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGC 1159
Qу
            Db
       1395 AGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAGC 1454
       1160 TGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
            1 1111111 1 111
                           Dh
       1455 TCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 1492
RESULT 14
US-10-028-158-20
; Sequence 20, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
  APPLICANT: Caniggia, Isabella
  APPLICANT: Post, Martin
  APPLICANT: Lye, Stephen
  TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
  TITLE OF INVENTION: TROPHOBLAST
  FILE REFERENCE: 11757.38USWO
  CURRENT APPLICATION NUMBER: US/10/028,158
  CURRENT FILING DATE: 2001-12-20
  PRIOR APPLICATION NUMBER: US/09/380,662
  PRIOR FILING DATE: 1999-12-21
  PRIOR APPLICATION NUMBER: PCT/CA98/00180
  PRIOR FILING DATE: 1998-03-05
 PRIOR APPLICATION NUMBER: US 60/039,919
 PRIOR FILING DATE: 1997-03-07
 NUMBER OF SEQ ID NOS: 24
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
   LENGTH: 2574
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (254)..(1492)
US-10-028-158-20
 Query Match
                     18.7%; Score 224.4; DB 13; Length 2574;
 Best Local Similarity 53.3%; Pred. No. 9.2e-53;
 Matches 660; Conservative 0; Mismatches 506; Indels
                                                      72; Gaps
                                                                 6;
Qу
         - 111
Db
        261 TGCACTTGCAAAGGGCTCTGGTGGTCCTGGCCCTGCTGAACTTTGCCACGGTCAGCCTCT 320
         86 GACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCA 145
Qу
             Db
        321 CTCTGTCCACTTGCACCACCTTGGACTTCGGCCACATCAAGAAGAAGAGGGTGGAAGCCA 380
        146 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 205
Qу
```

Db	381		440
Qу	206	CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG	265
Db	441	CCCACGTCCCCTATCAGGTCCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG	494
Qу	266	CCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGACTACT	310
Db	495		554
Qy	311	ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT	370
Db	555	ATGCCAAAGAAATCCATAAATTCGACATGATCCAGGGGCTGGCGGAGCACAACGAACTGG	614
Qy	371	TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG	430
Db	615	CTGTCTGCCCTAAAGGAATTACCTCCAAGGTTTTCCGCTTCAATGTGTCCTCAGTGGAGA	674
Qy	431	TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAG	490
Db	675	AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGGTGCCCAACCCCAGCT	734
Qy	491	TGGAGCACGTGGAGCTATACCAGAAATACAGCAATG	529
Db	735	CTAAGCGGAATGAGCAGAGGATCGAGCTCTTCCAGATCCTTCGGCCAGATGAGCACATTG	794
Qy	530	ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGCCCCCAGTGACTCACCGGAGTGGCTGT	589
Db	795	CCAAACAGCGCTATATCGGTGGCAAGAATCTGCCCACACGGGGCACTGCCGAGTGGCTGT	854
Qy	590	CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT	649
Db	855	CCTTTGATGTCACTGACACTGTGCGTGAGTGGCTGTTGAGAAGAGAGTCCAACTTAGGTC	914
Qy	650	TTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGG	703
Db	915	TAGAAATCAGCATTCACTGTCCATGTCACACCTTTCAGCCCAATGGAGATATCCTGGAAA	974
Qy	704	AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC	763
Db	975	ACATTCACGAGGTGATGGAAATCAAATTCAAAGGCGTGGACAATGAGGATGACCATGGCC	1034
Qу	764	GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGC	819
Db	1035	GTGGAGATCTGGGGCGCCTCAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCCTCA	1094
Qy	820	TCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGG	859
Db	1095	TGATGATTCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGTCAGAGGAAGAAGCGGG	1154
Qy	860	CCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	919
Db	1155	CTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCTCT	1214
Qy	920	ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATG	979

```
1215 ACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTATG 1274
Db
Qу
       980 CCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGG 1039
           11111
                                                   111111111
       1275 CCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACCCACAGCACGG 1334
Db
       Qу
           1 1111 1111111
                         1335 TGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCC 1394
Db
       1100 AGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGC 1159
Qу
           1395 AGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAGC 1454
Db
       1160 TGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           1455 TCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 1492
Dh
RESULT 15
US-09-906-158-10
; Sequence 10, Application US/09906158
: Publication No. US20030078217A1
; GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
  FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 10
   LENGTH: 2879
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (611) ... (1843)
US-09-906-158-10
 Query Match
                    18.4%; Score 220.4; DB 11; Length 2879;
 Best Local Similarity
                    52.1%; Pred. No. 1.3e-51;
 Matches 645; Conservative 0; Mismatches 521; Indels
                                                  72; Gaps
                                                             4;
QУ
        11
                     111
                                     612 TGCACTTGCAAAGGGCTCTGGTAGTCCTGGCCCTGCTGAACTTGGCCACAATCAGCCTCT 671
Db
        86 GACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCA 145
Qу
             672 CTCTGTCCACTTGCACCACGTTGGACTTCGGCCACATCAAGAAGAAGAGGGTGGAAGCCA 731
Db
        146 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCCGAGCCAGGGGGACGTGC 205
Qу
           732 TTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCATCGGTGATGA 791
Db
```

Qy	206	CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG	265
Db	792	CCCACGTCCCCTATCAGGTCCTGGCACTTTACAACAGCACCCGGGAGTTGCTGG	845
Qy	266	CCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGACTACT	310
Db	846		905
Qу	311	ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT	370
Db	906	ATGCCAAAGAGATCCATAAATTCGACATGATCCAGGGACTGGCGGAGCACAATGAACTGG	965
Qy	371	TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG	430
Db	966	CCGTCTGCCCCAAAGGAATTACCTCTAAGGTTTTTCGTTTCAATGTGTCCTCAGTGGAGA	1025
Qy	431	TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCA	481
Db	1026	AAAATGGAACCAATCTGTTCCGGGCAGAGTTCCGGGTCTTGCGGGTGCCCAACCCCAGCT	1085
Qy	482	AGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATG	529
Db	1086	CCAAGCGCACAGAGCAGAATTGAGCTCTTCCAGATACTTCGACCGGATGAGCACATAG	1145
Qy	530	ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGT	589
Db	1146	CCAAGCAGCGCTACATAGGTGGCAAGAATCTGCCCACAAGGGGCACCGCTGAATGGCTGT	1205
Qу	590	CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT	649
Db	1206	CTTTCGATGTCACTGACACTGTGCGCGAGTGGCTGTTGAGGAGAGAGTCCAACTTGGGTC	1265
Qу	650	TTCGCCTCAGTGCCCACTCTTCCTCTGACAGC	681
Db	1266	TGGAAATCAGCATCCACTGTCCATGTCACACCTTTCAGCCCAATGGAGACATACTGGAAA	1325
Qy	682	AAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACC	739
Db	1326	ATGTTCATGAGGTGATGGAAATCAAATTCAAAGGAGTGGACAATGAAGATGACCATGGCC	1385
Qy	740	TGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGA	799
Db	1386	GTGGAGACCTGGGGCGTCTCAAGAAGCAAAAGGATCACCACACCCACACCTGATCCTCA	1445
Qy	800	GGGCCCAGCACCTGCACAGCTCCCGGCACCCGCCGAGACTACAAGGATGACGACGACAAGG	859
Db	1446	TGATGATCCCCCCACACCGACTGGACAGCCCAGGCCAGG	1505
QУ	860	CCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	919
Db	1506	CCCTGGACACCAATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGTACGCCCCCTTT	1565
Qy	920	ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATG	979
Db	1566	ATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTTACTATG	1625
Qy	980	CCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGG	1039

Db	1626		1685
Qу	1040	TCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGTCGGCGCGCGC	1099
Db	1686	TGCTTGGACTATACAACACCCTGAACCCAGAGGCGTCTGCCTCGCCATGCTGCGTCCCCC	1745
Qy	1100	AGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGC	1159
Db	1746	AGGACCTGGAGCCCTGACCATCTTGTACTATGTGGGCAGAACCCCCAAGGTGGAGCAGC	1805
Qу	1160	TGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197	
Db	1806	TGTCCAACATGGTGGAAGTCGTGTAAGTGCAGCTGA 1843	

Search completed: October 28, 2003, 09:04:07

Job time : 362.927 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 2970.42 Seconds

(without alignments)

9794.056 Million cell updates/sec

Title: US-10-017-372E-8

Perfect score: 1197

Sequence: 1 atggcgccttcggggctgcg.....gttcctgcaagtgcagctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*

```
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mam:*
24: em_gss_pro:*
25: em_gss_pro:*
26: em_gss_pto:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
```

왕

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.			Query				
		Score	Match	Length	DB	ID	Description
	1	729	60.9	1072	12	BM562135	BM562135 AGENCOURT
C	2	692.2	57.8	1201	13	BX355682	BX355682 BX355682
С	3	685.8	57.3	983	13	BX335351	BX335351 BX335351
	4	682.4	57.0	900	13	BX349319	BX349319 BX349319
C	5	629.6	52.6	1041	13	BX324511	BX324511 BX324511
	6	629.4	52.6	1043	12	BM555996	BM555996 AGENCOURT
С	7	603.6	50.4	950	13	BX383773	BX383773 BX383773
C	8	589	49.2	888	13	BX434425	BX434425 BX434425
	9	577.2	48.2	859	9	AL530081	AL530081 AL530081
	10	569	47.5	713	10	BE312000	BE312000 601154768
	11	561.2	46.9	717	10	BE260971	BE260971 601153715
	12	556	46.4	902	13	BQ675698	BQ675698 AGENCOURT
	13	534.2	44.6	925	12	BI818841	BI818841 603037307
	14	521.2	43.5	1093	12	BQ054305	BQ054305 AGENCOURT
С	15	520.2	43.5	841	9	AL530080	AL530080 AL530080
C	16	520	43.4	956	12	BI084718	BI084718 602869722
	17	514	42.9	1049	12	BQ053417	BQ053417 AGENCOURT
	18	513.6	42.9	871	13	BQ952138	BQ952138 AGENCOURT
	19	506.4	42.3	1013	12	BM469326	BM469326 AGENCOURT
	20	504.6	42.2	943	12	BI909079	BI909079 603070060
	21	501.8	41.9	821	10	BG748049	BG748049 602705544
	22	491.8	41.1	773	12	BI195242	BI195242 602944518
С	23	488	40.8	1047	13	BX325288	BX325288 BX325288
	24	486.8	40.7	637	12	BG938856	BG938856 cn28g07.y
	25	482.8	40.3	748	10	BF682938	BF682938 602117568
С	26	482.2	40.3	757	14	CA309731	CA309731 UI-H-FT1-
	27	474.6	39.6	659	10	BG500488	BG500488 602544826

	28	472.8	39.5	675	10	BE261764	BE261764 601147839
					_		
	29	464.2	38.8	960	13	BU957001	BU957001 AGENCOURT
	30	460.2	38.4	599	12	BI905963	BI905963 603062849
С	31	455.2	38.0	727	9	AI131171	AI131171 qc15c11.x
	32	454.2	37.9	814	12	BI686959	BI686959 603313837
	33	453.4	37.9	633	14	CB577186	CB577186 AMGNNUC:N
С	34	453.2	37.9	785	9	AI148173	AI148173 qb56d01.x
	35	452.2	37.8	548	12	BM068788	BM068788 ie85a02.y
	36	449.8	37.6	982	13	BQ672677	BQ672677 AGENCOURT
	37	447.4	37.4	981	12	BM802192	BM802192 AGENCOURT
	38	445.8	37.2	588	13	BX097979	BX097979 BX097979
С	39	445.6	37.2	928	13	BX412434	BX412434 BX412434
	40	444.8	37.2	565	14	CD287835	CD287835 1_M15.abd
	41	442.4	37.0	636	10	BE615330	BE615330 601280728
С	42	439.6	36.7	722	13	BU632686	BU632686 UI-H-FE1-
С	43	437.6	36.6	695	14	CA425775	CA425775 UI-H-FE1-
С	44	436.6	36.5	700	13	BU633922	BU633922 UI-H-FL1-
C	45	436.4	36.5	1015	10	BG683840	BG683840 602651694

ALIGNMENTS

```
RESULT 1
BM562135
                                                        linear
LOCUS
                                    1072 bp
                                               mRNA
                                                                 EST 20-FEB-2002
            BM562135
DEFINITION AGENCOURT 6562032 NIH MGC 118 Homo sapiens cDNA clone IMAGE:5745463
            5', mRNA sequence.
ACCESSION
            BM562135
VERSION
            BM562135.1 GI:18807966
KEYWORDS
            EST.
SOURCE
            Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              (bases 1 to 1072)
REFERENCE
  AUTHORS
            NIH-MGC http://mgc.nci.nih.gov/.
  TITLE
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
  JOURNAL
            Contact: Robert Strausberg, Ph.D.
COMMENT
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12768 row: h column: 08
            High quality sequence start: 9
            High quality sequence stop: 647.
FEATURES
                     Location/Qualifiers
     source
                     1. .1072
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE: 5745463"
```

```
/tissue type="leukocyte"
               /lab host="DH10B"
               /clone_lib="NIH MGC 118"
               /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
               (destroyed); RNA source leukocytes from anonymous pool of
               non-activated adult donors. Library is oligo-dT primed
               and directionally cloned (EcoRV site is destroyed upon
               cloning). Average insert size 1.7 kb, insert size range
               1.2-3.3 kb. Library is normalized and enriched for
               full-length clones and was constructed by C. Gruber
               (Invitrogen). Research Genetics tracking code 027. Note:
               this is a NIH MGC Library."
           217 a
                        313 q
BASE COUNT
                  356 c
ORIGIN
 Query Match
                  60.9%; Score 729; DB 12; Length 1072;
 Best Local Similarity 83.6%; Pred. No. 1.7e-155;
                      0; Mismatches 145; Indels
                                              29; Gaps
                                                       4;
 Matches 885; Conservative
Qу
       117 GCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCT 176
          20 GCTGGTGAAGCGGAAGCGCATCTAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCT 79
Db
       Qу
           Db
       237 TCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCC 296
Qу
           140 CCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGACTGCAGAACCGGAGCCCGAGCC 199
Db
       297 AGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCA 356
Qу
           200 TGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGA 259
Db
       357 AATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGA 416
Qу
          Db
       417 GCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAG 476
Qу
          320 GCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAG 379
Db
       477 GCTCAAGTTAAAAGTGGAGCACCTGGAGCTATACCAGAAATACAGCAATGATTCCTG 536
Qу
```

Db

Qу

Db

Qу

Db

Qу

380 GCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTG 439

537 GCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGA 596

597 TGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCT 656

657 CAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTT 716

Db 56	0 TAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTT 619
Qy 71	7 CAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCT 776
Db 62	0 CACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCT 679
Qy 77	7 CCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGA 836
Db 68	0 TCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCG 736
Qy 83	7 CTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAA 896
Db 73	7AGCCCCTGGACACCAACTATTGCTTCAGCTCCCCGGAGAA 776
Qy 89	7 GAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGAT 956
Db 77	7 GAACTGCTGCGTGCGCAGCTGTACATTGACTTCCGCAGGGACCTCGGCTGGAAGTGGAT 836
Qy 95	7 TCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAG 1016
	7 CCACGAGCCCCAAGGCTACCATGCCCACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAG 896
-	7 CCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTC 1076
	7 CCTGGACACGCGTACCAGCAAGTCCCTGGCCCTGTACACCCGCCATAACCGGGCGCCCTC 956
-	7 GGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACG 1132
	7 GGCGGCGCGGGTTTGCTGGGCCCCAGGCCCCTGGACCCCCTGCCCCTTCGGGGTACTACC 1016
	3 TGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACAT 1169
Db 101	7 TGGGGCGCCAAGCCCCAAGTGGGAACACCTGTCCCACAT 1055
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	BX355682 1201 bp mRNA linear EST 05-MAY-2003 BX355682 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI002YJ05 3-PRIME, mRNA sequence. BX355682 BX355682.1 GI:30371987 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9160.r For

```
more information about this cluster, see
         http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0DI002CE03NP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
         http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID: CS0DI002CE03NP1.
FEATURES
                 Location/Oualifiers
                 1. .1201
    source
                 /organism="Homo sapiens"
                 /mol type="mRNA"
                 /db xref="taxon:9606"
                 /clone="CS0DI002YJ05"
                 /tissue type="PLACENTA COT 25-NORMALIZED"
                 /clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                 /note="1st strand cDNA was primed with a NotI-oligo(dT)
                 primer. Five prime end enriched, double-strand cDNA was
                 digested with Not I and cloned into the Not I and EcoR V
                 sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
             198 a
                    326 c
                            386 g
                                           38 others
                                   253 t
ORIGIN
 Query Match
                     57.8%; Score 692.2; DB 13; Length 1201;
                     86.7%; Pred. No. 4.2e-147;
 Best Local Similarity
 Matches 824; Conservative
                           4; Mismatches
                                        93;
                                            Indels
                                                    29; Gaps
                                                               5;
        250 ACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG-GCGGACTA 308
Qу
           Db
       1046 AACCGCGACCGGGTGGCCGGG--AGAKKCAGAACCGGAGCCCGAGCCTGAGCCCGRACTA 989
Qу
        309 CTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAA 368
            Db
        988 CTACGCCAAGGAGGTMACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATGACAA 929
Qу
        369 ATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGC 428
                      928 GTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGC 869
Db
        429 GGTGCCGGAACCTGTATTGCTCT-CTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAA 487
Qу
            Db
        868 GGTACCTGAACCCGTGTTGCTCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAA 809
Qу
        488 AAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCA 547
           Db
        808 AAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGATACCTCA 749
Qу
        548 GCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAG 607
           748 GCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAG 689
Db
        608 TTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACT 667
Qу
           Db
        688 TTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGA-GGCTTTCGCCTTAGCGCCCACT 630
Qу
        668 CTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCC 727
             Db
        629 GCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCC 570
```

Qy 728	GCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCA 787
Db 569	
Qy 788	CCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATG 847
Db 509	
Qy 848	ACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCG 907
Db 462	
Qy 908	TGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCA 967
Db 413	TGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCA 354
Qy 968	AGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTC 1027
Db 353	AGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGC 294
Qy 1028	AGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGC
Db 293	AGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGCGCCCCT 234
Qy 1088	GCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCA 1147
Db 233	GCTGCGTGCCGCAGGCGCTGGAGCCCATCGTGTACTACGTGGGCCGCAAGCCCA 174
Qy 1148	AGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Db 173	AGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 124
DEFINITION BY COMMENT COMMENT COMMENT	X335351 983 bp mRNA linear EST 01-MAY-2003 X335351 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA lone CS0DI013YH16 3-PRIME, mRNA sequence. X335351 X335351.1 GI:30308367 ST. Domo sapiens (human) Domo sapiens Unkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Dammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 983) i,W.B., Gruber,C., Jessee,J. and Polayes,D. Dull-length cDNA libraries and normalization Dupublished Domact: Genoscope Denoscope - Centre National de Sequencage Denoscope -

```
URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
         Faraday Avenue Genoscope sequence ID : CS0DI013DD08NP1.
                Location/Qualifiers
FEATURES
                1. .983
   source
                /organism="Homo sapiens"
                /mol type="mRNA"
                /db xref="taxon:9606"
                /clone="CS0DI013YH16"
                /tissue type="PLACENTA COT 25-NORMALIZED"
                /clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="lst strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
            170 a
                    280 c
                           323 q
                                  203 t
                                           7 others
ORIGIN
 Query Match
                    57.3%; Score 685.8; DB 13; Length 983;
 Best Local Similarity
                    86.6%; Pred. No. 1.1e-145;
 Matches 805; Conservative
                         5; Mismatches
                                       93; Indels
                                                   27; Gaps
                                                             4;
0v
        268 GGGGAAAGTGTCGAACCGGAGCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACC 327
                    983 GGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGCCGACTACTACGCCAAGGAGGTCACC 924
Db
        328 CGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCCAC 387
Qу
           923 CGCGTGCTAATGGTGGARACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACACAC 864
Db
        388 AGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTG 447
Qу
           Db
        863 AGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTG 804
        448 CTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCACGTGGAG 507
Qy
           803 CTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCACGTGGAG 744
Db
        508 CTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCC 567
Qу
           743 CTGTACCAGAAATACAGCAACAATYCCTGGCGATACCTCAGCAACCGGCTGCTGGCACCC 684
Db
        568 AGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACC 627
Qу
           683 AGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGC 624
Db
        628 CGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGAT 687
Qу
              623 CGTGGAGGGGAAATTGA-GGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGAT 565
ďÚ
        688 AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC 747
Qу
           564 AACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCGGGGTGACCTGGCCACC 505
Db
        748 ATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAG 807
Qу
```

504 ATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCGGTGGAGAGGGCCCAG 445

Db

&cluster=9160.r. Contact : Feng Liang Email : fliang@lifetech.com

```
808 CACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGGAT 867
Qу
           Db
        444 CATCTGCAAAGCTCCCGGCACCGCCGA-------GCCCTGGAC 409
Qу
        Db
        Qу
        928 TTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTC 987
           Db
        348 TTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTC 289
        988 TGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCT 1047
Qу
           Db
        288 TGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTAMMMCAAGGTCCTGGCC 229
       1048 CTGTACAACCAGCACAACCCGGGCGCGTCGGCGCGCGCGTGCTGCCGCAGGCGCTG 1107
Qу
           Db
        228 MTGTACAACCAGCATAACCC-GGCGCCTCGGCGGCGCCGTNGT-CGTGCCGCAGGCGCTG 171
       1108 GAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 1167
Qу
           Db
        170 GAGCCGCTGCCCATCGTGTACTACGTGGGCTGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 111
       1168 ATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
Qу
           Db
        110 ATGATCGTGCGCTCCTGCAAGTGCAGCTGA 81
RESULT 4
BX349319
LOCUS
         BX349319
                             900 bp
                                     mRNA
                                           linear
                                                   EST 05-MAY-2003
DEFINITION BX349319 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
         Homo sapiens cDNA clone CS0DL010YL07 5-PRIME, mRNA sequence.
ACCESSION
         BX349319
         BX349319.1 GI:30379410
VERSION
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM
         Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
           (bases 1 to 900)
 AUTHORS
         Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
         Full-length cDNA libraries and normalization
 JOURNAL
         Unpublished
COMMENT
         Contact: Genoscope
         Genoscope - Centre National de Sequencage
         BP 191 91006 EVRY cedex - France
         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
         Library was constructed by Life Technologies, a division of
         Invitrogen. This sequence belongs to sequence cluster 9160.r For
         more information about this cluster, see
         http://www.genoscope.cns.fr/
         cgi-bin/cluster.cgi?seq=CS0BAG059ZD04_CS05596_1&cluster=9160.r.
         Contact : Feng Liang Email : fliang@lifetech.com URL :
         http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
```

```
Faraday Avenue Genoscope sequence ID : CS0BAG059ZD04 CS05596 1.
FEATURES
               Location/Qualifiers
               1. .900
   source
               /organism="Homo sapiens"
               /mol type="mRNA"
               /db_xref="taxon:9606"
               /clone="CSODL010YL07"
               /cell type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
               /cell line="RAMOS CELL LINE"
               /clone lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
               25-NORMALIZED"
               /note="1st strand cDNA was primed with a NotI-oligo(dT)
               primer. Five prime end enriched, double-strand cDNA was
               digested with Not I and cloned into the Not I and EcoR V
               sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
           179 a
                  292 c
                        270 q
                              155 t
                                       4 others
ORIGIN
 Query Match
                  57.0%; Score 682.4; DB 13; Length 900;
 Best Local Similarity 88.4%; Pred. No. 6.4e-145;
 Matches 740; Conservative
                       0; Mismatches
                                   97;
                                       Indels
                                               0; Gaps
                                                       0;
        Ov
          Db
        61 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qy
          95 CTGACGCCTGGCCGGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 154
Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
          155 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 214
Db
       181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
Qу
          215 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 274
Db
       241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300
Qу
          Db
       301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360
Qу
          335 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 394
Db
       361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420
Qу
          Db
       395 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 454
       421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480
Qу
          455 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 514
Db
       481 AAGTTAAAAGTGGAGCACCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540
Qу
          Db
       515 AAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 574
```

```
Qу
        541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 600
            Db
        575 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTC 634
Qу
        601 ACCGGAGTTGTGCGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT 660
            Db
         635 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 694
        661 GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 720
Qy
            Db
        695 GCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACT 754
        721 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qу
             755 ACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTTCTGCTTCTC 814
Db
        781 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC 837
Qу
            Db
        815 ATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGNCGAGCC 871
RESULT 5
BX324511/c
LOCUS
          BX324511
                               1041 bp
                                         mRNA
                                                linear
                                                        EST 02-MAY-2003
DEFINITION BX324511 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
          cDNA clone CS0DC024YD20 3-PRIME, mRNA sequence.
ACCESSION
          BX324511
VERSION
          BX324511.1 GI:30332381
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 1041)
 AUTHORS
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
          Unpublished
COMMENT
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 9160.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cqi-bin/cluster.cqi?seq=CS0AC024DB10NP2&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CSOACO24DB10NP2.
FEATURES
                  Location/Qualifiers
    source
                  1. .1041
                  /organism="Homo sapiens"
                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="CS0DC024YD20"
                  /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
```

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 176 a 283 c 346 g 219 t 17 others ORIGIN

	ocal :	52.6%; Score 629.6; DB 13; Length 1041; Similarity 84.7%; Pred. No. 7.1e-133; 8; Conservative 8; Mismatches 102; Indels 32; Gaps	7;
Qy	269	GGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGGGGACTACTACGCCAAGGAGGTCACCC 32	28
Db	1022	SGGGAGAKGSAGAACCGGAGCCCGACCCTRASCCRACTAYACCCCAAGRAGTCACCC 96	66
Qy	329	GCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCCACA 38	88
Db	965	GCGTGYTAATGKT-GAAACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACACACA 90	07
Qy	389	GCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTGC 44	48
Db	906	GCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTGC 84	47
Qy	449	TCTCTC-GGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAG 50	07
Db	846	TCTCCCSGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCACGTGGAG 78	87
Qy	508	CTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCC 56	б7
Db	786	CTGTACCAGAAATACAGCAACAATTCCTGGCGATACCTCAGCAACCGGCTGCTGGCACCC 72	27
Qy	568	AGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACC 62	27
Db	726	AGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGC 66	67
Qy	628	CGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGAT 68	87
Db	666	CGTGGAGGGGAAATTGA-GGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGAT 60	80
Qy	688	AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC 74	47
Db	607	AACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCACC 54	48
Qy	748	ATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAG 8 C	07
Db	547	ATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCCAG 48	88
QУ		CACCIGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGGAT 86	
Db	487	CATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGGAC 45	52
Qy	868	ACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	27
Db	451	ACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	92
Qy	928	TTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTC 98	37

```
Db
        391 TTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTC 332
Qу
        988 TGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCT 1047
            Db
        331 TGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCC 272
Qу
        1048 CTGTACAACCAGCACAACCCGGGCGCGTCGGCGCGCGCGTGCTGCCGCAGGCGCTG 1107
            Db
        271 CTGTACAACCAGCATAACCC-GGCGCCCTCGGCGCGCGCGTG-TGCGTGCCGCAGGCGCTG 214
Qу
        1108 GAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 1167
            213 GAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 154
Db
Qу
        1168 ATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1197
            Db
        153 ATGATCGTGCGCTCCTGCAAGTGCAGCTGA 124
RESULT 6
BM555996
LOCUS
          BM555996
                                1043 bp
                                         mRNA
                                                linear EST 20-FEB-2002
DEFINITION AGENCOURT 6544437 NIH MGC_88 Homo sapiens cDNA clone IMAGE:5550039
          5', mRNA sequence.
          BM555996
ACCESSION
          BM555996.1 GI:18796907
VERSION
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
          1 (bases 1 to 1043)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM12261 row: i column: 16
          High quality sequence stop: 702.
FEATURES
                  Location/Qualifiers
                  1. .1043
    source
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db xref="taxon:9606"
                  /clone="IMAGE:5550039"
                  /tissue type="duodenal adenocarcinoma, cell line"
                  /lab_host="DH10B (phage-resistant)"
                  /clone lib="NIH MGC 88"
                  /note="Organ: small intestine; Vector: pCMV-SPORT6;
```

Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 202 a 329 c 345 g 154 t $1\overline{3}$ others ORIGIN

	cal	52.6%; Score 629.4; DB 12; Length 1043; Similarity 88.1%; Pred. No. 7.9e-133; 6; Conservative 0; Mismatches 71; Indels 24; Gaps	1;
Qу	386	ACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTAT	445
Db	1	ACAGCATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGT	60
Qу	446	TGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGG	505
Db	61	TGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCACGTGG	120
Qy	506	AGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCC	565
Db	121	AGCTGTACCAGAAATACAGCAACAATTCCTGGCGATACCTCAGCAACCGGCTGCTGGCAC	180
Qy	566	CCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGA	625
Db	181	CCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGA	240
Qу	626	CCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAG	685
Db	241	GCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGG	300
Qy	686	ATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCA	745
Db	301	ATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCA	360
Qy	746	CCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCC	805
Db	361	CCATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCC	420
Qу		AGCACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGG	
Db	421	AGCATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGG	456
Qу	866	ATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	925
Db	457	ACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	516
Qу	926	ACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATT	985
Db	517	ACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACT	576
Qy	986	TCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGG	1045
Db	577	TCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGG	636
Qу	1046	CTCTGTACAACCAGCACAACCCGGGCGCGTCGGGCGCGCGC	1105

```
Db
         637 CCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGC 696
Qу
         1106 TGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA 1165
              Db
         697 TGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA 756
         1166 ACATGATCGTGCGTTCCTGCA 1186
Qу
              111111111
Db
         757 ACATGATCGTGCGCTCCTGCA 777
RESULT 7
BX383773/c
LOCUS
           BX383773
                                    950 bp
                                             mRNA
                                                      linear
                                                              EST 08-MAY-2003
DEFINITION BX383773 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
           cDNA clone CS0DK001YA15 3-PRIME, mRNA sequence.
ACCESSION
           BX383773
           BX383773.1 GI:30457168
VERSION
KEYWORDS
           EST.
SOURCE
           Homo sapiens (human)
 ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
           1 (bases 1 to 950)
 AUTHORS
           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
           Full-length cDNA libraries and normalization
 TITLE
  JOURNAL
           Unpublished
           Contact: Genoscope
COMMENT
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. This sequence belongs to sequence cluster 9160.r For
           more information about this cluster, see
           http://www.genoscope.cns.fr/
           cgi-bin/cluster.cgi?seq=CS0DK001AA08NP1&cluster=9160.r. Contact :
           Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
           Faraday Avenue Genoscope sequence ID : CSODKOO1AA08NP1.
FEATURES
                    Location/Qualifiers
                    1. .950
    source
                    /organism="Homo sapiens"
                    /mol type="mRNA"
                    /db xref="taxon:9606"
                    /clone="CS0DK001YA15"
                    /cell type="HELA CELLS COT 25-NORMALIZED"
                    /cell line="HELA"
                    /clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                    /note="1st strand cDNA was primed with a NotI-oligo(dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
               171 a
                        260 c
                                 312 g
                                         195 t
                                                   12 others
ORIGIN
 Query Match
                         50.4%; Score 603.6; DB 13; Length 950;
 Best Local Similarity
                         83.9%; Pred. No. 5.7e-127;
```

Matches	717	7;	Conservative	8;	Mismat	ches	104;	Indels	26;	Gaps	3;
Qy	343		AAGCGGCAACCAAATC								402
Db	943		 AACCCACAACGAAATO								884
Qy	403		CAACACGTCGGAGCTC								462
Db	883		CAAMACATCAGAGCTO								824
Qy	463		GCGCCTGCTGAGGCT(522
Db	823		GCGTCTGCTGAGGCTC								764
Qy	523		CAATGATTCCTGGCGC								582
Db	763		CAACAATAMCTGGCGA								704
Qy	583	TG(GCTGTCCTTTGATGTC						AGAGAG	GCTATA	642
Db	703	TG	GTTATCTTTTGATGTC							GAAATT	644
Qy	643		GGGTTTTCGCCTCAG1			CTCTG#		_	ACACTC		702
Db	643		-ĠĠĊŤŦŤĊĠĊĊŤŦĂĠĊ								585
Qy	703		AATTAACGGGTTCAAT								762
Db	584	GA	CATCAACGGGTTTACT	raccg(geegeeg.	AGGTGA	ACCTGG	CCACCATT	CATGGC	ATGAAC	525
Qy	763		GCCCTTCCTGCTCCT(CCCAGCAC(822
Db	524	CG	GCCTTTCCTGCTTCTC	CATGG	CCACCCC	GCTGG	AGAGGG	CCAGCATO	CTGCAA	AGCTCC	465
Qу			GCACCGCCGAGACTAC 				1.1 1			11111	
Db								rggacacc <i>i</i>			
Qy	883	AG(CTCCACGGAGAAGAAC	TGCT 	GCGTGCG 	GCAGCT	CTACAT	TTGACTTC(:	CGGAAG	GACCTG	942
Db		AG	CTCCACGGAGAAGAAC	CTGCT(GCGTGCG	GCAGCT	rgtaca?	TKACTTC	CGCAAG	GACCTC	
Qу		11	CTGGAAGTGGATTCAT			111111			11 111	11111	
Db			CTGGAAGTGGATCCAC								
			CTACATCTGGAGCCTA	HHI		11111		111 1			
dio			CTACATTTGGAGCCTG								
_			CCCGGGCGCGTCGGCG	1111		[[]]	11111	11111111			
Db			ACCCGGCGCCTCGGCG								
_		11	GTACTACGTGGGCCGC	1111	111111	111111	111111	1 111111	11111	11 111	
Db	189	G'I'(GTACTACGTGGGCKKC	:AAGC(CAAGGT	GAGCA	GCTGTC	CNACATGA	A'TCGTG(CGCTCC	130

```
Qу
         1183 TGCAAGTGCAGCTGA 1197
              111111111111
Db
          129 TGCAAGTGCAGCTGA 115
RESULT 8
BX434425/c
LOCUS
            BX434425
                                     ad 888
                                               mRNA
                                                       linear
                                                                EST 15-MAY-2003
DEFINITION
            BX434425 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE014YE16
            3-PRIME, mRNA sequence.
ACCESSION
            BX434425
VERSION
            BX434425.1 GI:30779291
KEYWORDS
            EST.
SOURCE
            Homo sapiens (human)
  ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               (bases 1 to 888)
REFERENCE
  AUTHORS
            Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  TITLE
            Full-length cDNA libraries and normalization
  JOURNAL
            Unpublished
COMMENT
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 9160.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cqi-bin/cluster.cqi?seq=CS0BAK028AB08NM1&cluster=9160.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAK028AB08NM1.
FEATURES
                     Location/Qualifiers
     source
                     1. .888
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="CS0DE014YE16"
                     /tissue type="PLACENTA"
                     /clone lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
BASE COUNT
                156 a
                         253 C
                                  302 g
                                           176 t
                                                      1 others
ORIGIN
  Query Match
                          49.2%; Score 589; DB 13; Length 888;
  Best Local Similarity
                          87.1%; Pred. No. 1.2e-123;
  Matches 679; Conservative
                               0; Mismatches
                                                 76; Indels
                                                                25;
                                                                     Gaps
                                                                             2;
Qу
          418 CTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGG 477
              1111
                     111111 11 1111 1 111
```

888 CTCCAAAAAGCGGTACCTGAACCCTTGTTGTCTNCCCGGGCAGAGCTGCGTCTGCTGA-G 830

Db

Qy	478	CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG	537
Db	829	CTCAAGTTTAAAATGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG	770
Qу	538	CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT	597
Db	769		710
Qу	598	GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC	657
Db	709		650
Qy	658	AGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC	717
Db	649	AGCGCCCACTGCTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC	590
Qy	718	AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	777
Db	589	ACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT	530
Qу	778	CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC	837
Db	529	CTCATGGCCACCCGGTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA	473
Qy	838	TACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAG	897
Db	472	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAG	434
Qу	898	AACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATT	957
Db	433	AACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATC	374
Qy	958	CATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGC	1017
Db	373	CACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGC	314
Qy	1018	CTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCG	1077
Db	313	CTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCG	254
QУ	1078	GCGGCGCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGC	1137
Db	253	GCGGCGCCGTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGC	194
Qy	1138	CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA	1197
Db	193	CGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA	134
RESULT 9 AL530081			

859 bp

DEFINITION AL530081 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA clone CS0DD009YM06 5-PRIME, mRNA sequence.

mRNA

LOCUS

VERSION

AL530081

AL530081.2 GI:31067916

ACCESSION AL530081

linear EST 23-MAY-2003

```
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM
          Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 859)
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 AUTHORS
          Full-length cDNA libraries and normalization
 TITLE
 JOURNAL
          Unpublished
COMMENT
          On Feb 13, 2001 this sequence version replaced gi:12793574.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          9160.r For more information about this cluster, see
          http://www.genoscope.cns.fr/
          cqi-bin/cluster.cqi?seq=CS0DD009BG03QP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DD009BG03QP1.
                  Location/Qualifiers
FEATURES
                  1. .859
    source
                  /organism="Homo sapiens"
                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="CS0DD009YM06"
                  /tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
                  /clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
                  primer. Five prime end enriched, double-strand cDNA was
                  digested with Not I and cloned into the Not I and EcoR {\tt V}
                  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
             179 a
                     272 c
                             257 g
                                    148 t
                                              3 others
ORIGIN
                      48.2%; Score 577.2; DB 9; Length 859;
 Query Match
 Best Local Similarity
                      87.3%; Pred. No. 5.6e-121;
 Matches 641; Conservative
                            2; Mismatches
                                           90;
                                              Indels
                                                       1; Gaps
                                                                  1;
Qу
          Db
        Qy
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
            186 CTGACGCCTGGCCGGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 245
Db
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
Qу
            Db
        246 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 305
Qу
        181 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240
            306 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 365
Db
```

Qy	241 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300)
Db		I
Qy	301 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360	ł
Db	426 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 485	i
Qy	361 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420	l
Db	486 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 545)
Qy	421 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480)
Db	546 CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 605	,
Qу	481 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540)
Db	606 AAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 665	1
Qy	541 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTG-GCTGTCCTTTGATGT 599	ı
Db	666 TACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGTGTTATCTTTTGATGT 725	,
Qу	600 CACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAG 659)
Db	726 CACCGGAGTTGTGCGCCAGTKGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAG 785	
Qy Db	660 TGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAA 719	
Qу	720 TTCTGGCCGCGGG 733	
Db		
RESULT 10 BE312000 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISH REFERENCE AUTHORS	mRNA sequence. BE312000 BE312000.1 GI:9130128 EST. Homo sapiens (human)	· O
TITLE JOURNAL COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory	

```
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM195 row: h column: 17
          High quality sequence start: 2
          High quality sequence stop: 713.
FEATURES
                 Location/Qualifiers
                 1. .713
    source
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db xref="taxon:9606"
                 /clone="IMAGE:3510592"
                 /tissue type="neuroblastoma"
                 /lab host="DH10B (phage-resistant)"
                 /clone lib="NIH MGC 19"
                 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
                 EcoRI; cDNA made by oligo-dT priming. Directionally
                 cloned into EcoRI/XhoI sites using the following 5'
                 adaptor: GGCACGAG(G). Library constructed by Ling Hong
                 in the laboratory of Gerald M. Rubin (University of
                 California, Berkeley) using ZAP-cDNA synthesis kit
                 (Stratagene) and Superscript II RT (Life Technologies).
                 Note: this is a NIH MGC Library."
BASE COUNT
             157 a
                     226 c
                            211 g
                                    119 t
ORIGIN
 Query Match
                     47.5%; Score 569; DB 10; Length 713;
                     87.4%; Pred. No. 3.9e-119;
 Best Local Similarity
 Matches 623; Conservative
                           0; Mismatches
                                                      0; Gaps
                                          90; Indels
                                                                 0;
        125 AGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCC 184
Qу
            1 AGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAGCC 60
Db
        185 CCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACA 244
Qу
            Db
         61 CCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTGTACA 120
        245 ACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGG 304
Qу
            Db
        121 ACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGCCG 180
        305 ACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATG 364
Qу
            Db
        181 ACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATG 240
        365 ATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGG 424
Qу
                           Db
        241 ACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAG 300
Qу
        425 AAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGT 484
            Db
        301 AAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGT 360
        485 TAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACC 544
Qу
```

```
Db
        361 TAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGATACC 420
Qу
        545 TCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCG 604
            Db
        421 TCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCG 480
        605 GAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGGTTTTCGCCTCAGTGCCC 664
QУ
            481 GAGTTGTGCGCCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGCGCCC 540
Dh
         665 ACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTG 724
Qу
            541 ACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCG 600
Db
         725 GCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGG 784
Qу
            Db
        601 GCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGG 660
        785 CCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGAC 837
Οv
            661 CCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCCGGCACCGCGAGCC 713
Db
RESULT 11
BE260971
LOCUS
                                717 bp
                                         mRNA
                                                linear
                                                        EST 26-OCT-2000
DEFINITION 601153715F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE:3509931 5',
          mRNA sequence.
ACCESSION
          BE260971
VERSION
          BE260971.1 GI:9132709
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM
          Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 717)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
          Contact: Robert Strausberg, Ph.D.
COMMENT
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM193 row: m column: 04
          High quality sequence stop: 713.
FEATURES
                  Location/Qualifiers
    source
                  1. .717
                  /organism="Homo sapiens"
                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="IMAGE:3509931"
                  /tissue type="neuroblastoma"
                  /lab host="DH10B (phage-resistant)"
```

/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

BASE COUNT 158 a 226 c 213 g 120 t ORIGIN

	Query Ma Best Loc	atch	46.9%; Score 561.2; DB 10; Length 717; Similarity 88.1%; Pred. No. 2.3e-117;	
	Matches	622	2; Conservative 0; Mismatches 83; Indels 1; Gaps	1;
Q	У	126	GCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCC 1	.85
D	b	1	GCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAGCCC 6	0
Q	У	186	CCCGAGCCAGGGGGACGTGCCGGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAA 2	45
D	b	61	CCCGAGCCAGG-GGAGGTGCCGGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTGTACAA 1	19
Q	У	246	CAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGA 3	05
D	b	120	CAGCACCCGCGACCGGGTGGCCGGGGAGACCGGAGCCCGAGCCTGAGGCCGA 1	.79
Q	У	306	CTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGA 3	65
D	b	180	CTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATGA 2	39
Q	У	366	TAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGA 4	25
D	b	240		99
Ç	У	426	AGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTT 4	85
D	b	300	AGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTT 3	59
Q	У	486	AAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCT 5	45
D	b	360	AAAAGTGGAGCAGCATGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGATACCT 4	19
Q	У	546	CAGCAACCGGCTGCTCGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGG 6	05
D	b	420	CAGCAACCGGCTGCCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGG 4	79
Q	У	606	AGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCA 6	65
D	р	480	AGTTGTGCGGCAGTGGTTGAGCCCTGGAGGGGAAATTGAGGGCTTTCGCCTTAGCGCCCA 5	39
Q	У	666	CTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGG 7	25
D	b	540		99
Q	У	726	CCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGC 7	85

```
Db
         600 CCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGC 659
         786 CACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGC 831
Qу
             Db
         660 CACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGC 705
RESULT 12
BQ675698
LOCUS
           BQ675698
                                   902 bp
                                             mRNA
                                                             EST 15-JUL-2002
                                                    linear
DEFINITION AGENCOURT 8036532 NIH MGC 102 Homo sapiens cDNA clone IMAGE:6211917
           5', mRNA sequence.
ACCESSION
           BQ675698
VERSION
           BQ675698.1 GI:21786532
KEYWORDS
           EST.
SOURCE
           Homo sapiens (human)
 ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 902)
           NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
           National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2375 row: c column: 22
           High quality sequence stop: 599.
FEATURES
                    Location/Qualifiers
                    1. .902
     source
                    /organism="Homo sapiens"
                    /mol type="mRNA"
                    /db xref="taxon:9606"
                    /clone="IMAGE:6211917"
                    /tissue type="epidermoid carcinoma, cell line"
                    /lab_host="DH10B (phage-resistant)"
                    /clone lib="NIH MGC 102"
                    /note="Organ: salivary gland; Vector: pOTB7; Site 1: XhoI;
                    Site 2: EcoRI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G). Library constructed
                    by Ling Hong in the laboratory of Gerald M. Rubin
                    (University of California, Berkeley) using ZAP-cDNA
                    synthesis kit (Stratagene) and Superscript II RT (Life
                    Technologies). Note: this is a NIH MGC Library."
BASE COUNT
               194 a
                        292 C
                                255 g
                                         161 t
ORIGIN
 Query Match
                        46.4%; Score 556; DB 13; Length 902;
 Best Local Similarity
                        87.7%; Pred. No. 3.8e-116;
```

Matches	60	7; Conservative	0;	Mismatches	85;	Indels	0;	Gaps	0;
Qy	146	TTCGCGGCCAGATTCTG							205
Db	1	 TCCGCGGCCAGATCCTG							60
Qу	206	CGCCCGCCCGCTGCCT				CAGTACCCGC			265
Db	61	CGCCCGGCCCGCTGCCC							120
Qy	266	CCGGGGAAAGTGTCGAA							325
Db	121	CCGGGGAGAGTGCAGAA							180
Qy	326	CCCGCGTGCTAATGGTG		CGGCAACCAAAT				CCCCCC	385
Db	181	CCCGCGTGCTAATGGTG						GTACAC	240
Qy	386	ACAGCTTATATATGCTG							445
Db	241	ACAGCATATATATGTTC							300
Qy	446	TGCTCTCTCGGGCAGAG							505
Db	301	TGCTCTCCCGGGCAGAG							360
Qy	506	AGCTATACCAGAAATAC							565
Db	361	AGCTGTACCAGAAATAC							420
Qy	566	CCAGTGACTCACCGGAG		GTCCTTTGATGT(625
Db	421	CCAGCGACTCGCCAGAG							480
Qy	626	CCCGCAGAGAGGCTATA		TTTTCGCCTCAG			GACA		685
Db	481	GCCGTGGAGGGGAAATT							540
Qy	686	ATAACACACTCCACGTG		TAACGGGTTCAAT					745
Db	541	ATAACACACTGCAAGTG							600
Qy	746	CCATTCACGGCATGAAC	CGGCC	CTTCCTGCTCCTC	CATGGC			GGGCCC	805
Db	601	CCATTCATGGCATGAAC	CGGCC	TTTCCTGCTTCTC	CATGGC				660
Qy	806	AGCACCTGCACAGCTCC		CCGCCGAGAC 83	37				
Db	661	AGCATCTGCCAAGCTCC			92				
RESULT 13 BI818841									

DEFINITION 603037307F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178433 5', mRNA sequence.

925 bp mRNA linear EST 04-OCT-2001

LOCUS BI818841

ACCESSION BI818841

```
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 925)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11444 row: n column: 02
          High quality sequence stop: 874.
FEATURES
                  Location/Qualifiers
                  1. .925
    source
                  /organism="Homo sapiens"
                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="IMAGE:5178433"
                  /lab host="DH10B"
                  /clone lib="NIH MGC 115"
                  /note="Organ: pooled brain, lung, testis; Vector:
                  pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                  source anonymous pool of 6 male brains, age range 23-27; 1
                  male lung, age 27; and 1 male testis, age 69. Library is
                  oligo-dT primed and directionally cloned (EcoRV site is
                  destroyed upon cloning). Average insert size 1.8 kb,
                  insert size range 1-3 kb. Library is normalized and
                  enriched for full-length clones and was constructed by C.
                  Gruber (Invitrogen). Research Genetics tracking code
                  021. Note: this is a NIH MGC Library."
BASE COUNT
             170 a
                     316 c
                             278 g
                                     161 t
ORIGIN
 Query Match
                      44.6%; Score 534.2; DB 12; Length 925;
 Best Local Similarity 87.6%; Pred. No. 3.5e-111;
 Matches 607; Conservative 0; Mismatches 83; Indels
                                                        3; Gaps
                                                                  2;
Qу
          Db
         61 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 120
Qу
            Db
        211 CTGACGCCTGGCCGGCCGCCGCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 270
Qу
        121 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 180
            Db
        271 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 330
```

BI818841.1 GI:15930391

VERSION

Qy		1 AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 240						
Db		1 AGCCCCCGAGCCAGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 390						
QУ		1 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 300						
Db	39	1 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 450						
Qy	30	1 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 360						
Db	45	1 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 510						
Qy	36	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 420						
Db	51							
Qy	42	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 480						
Db	57							
Qy	48	1 AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 540						
Db	63							
Qy	54	1 TACCTCAGCAACCGGCTGC-TGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGT 599						
Db	69							
Qy	60	CACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTC 657						
Db	75							
Qy	65	3 AGTGCCCACTCTTCCTCTGACAGCAAAGATAAC 690 						
Db	81	AGCGCCCACTGCTCCTGTGACAGCAGGGATACC 843						
RESULT 14 BQ054305								
LOCUS DEFINITION	N .	3Q054305 1093 bp mRNA linear EST 29-MAR-2002 AGENCOURT_6830409 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936397						
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	M	5', mRNA sequence. 3Q054305 3Q054305.1 GI:19813645 EST. Homo sapiens (human) Homo sapiens						
REFERENCE AUTHORS TITLE JOURNAL COMMENT	11 11 11 11 11 11 11 11 11 11 11 11 11	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1093) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Daniel McVicar, DBS/NCI						

```
cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM2125 row: k column: 22
          High quality sequence stop: 605.
FEATURES
                  Location/Qualifiers
                  1. .1093
    source
                  /organism="Homo sapiens"
                  /mol type="mRNA"
                  /db xref="taxon:9606"
                  /clone="IMAGE:5936397"
                  /tissue type="natural killer cells, cell line"
                  /lab host="DH10B (phage-resistant)"
                  /clone lib="NIH MGC 106"
                  /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
                  EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGCACGAG(G). Library constructed by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of California,
                  Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH MGC Library."
BASE COUNT
                      347 c
                                     203 t
              233 a
                             309 q
                                               1 others
ORIGIN
 Query Match
                       43.5%; Score 521.2; DB 12; Length 1093;
 Best Local Similarity 87.8%; Pred. No. 3.4e-108;
 Matches 590; Conservative 0; Mismatches
                                           58; Indels
                                                        24; Gaps
Qу
         525 CAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTG 584
                Db
          1 CAACAATTCCTGGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTG 60
         585 GCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGA 644
Qу
            Db
         61 GTTATCTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGA 120
         645 GGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGA 704
Qу
            Db
         121 GGGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGA 180
         705 AATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCG 764
QУ
             Db
         181 CATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCG 240
         765 GUUCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCG 824
ÛУ
            Db
         241 GCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCG 300
        825 GCACCGCCGAGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAG 884
Qу
                                          1111111 111111111 1111111
            Db
        301 GCACCGCCGA-----
                                     -----GCCCTGGACACCAACTATTGCTTCAG 336
Qу
        885 CTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGG 944
```

```
Db
         337 CTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGG 396
Qу
        945 CTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCC 1004
            Db
        397 CTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCC 456
QУ
        1005 CTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAA 1064
            457 CTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAA 516
Db
Qу
        Db
        517 CCCGGGCGCCTCGGCGGCGCCGTGCTGCGCAGGCGCTGGAGCCGCTGCCCATCGT 576
Qу
       1125 GTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTG 1184
            Db
        577 GTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTG 636
Qу
        1185 CAAGTGCAGCTG 1196
            Db
        637 CAAGTGCAGCTG 648
RESULT 15
AL530080/c
LOCUS
          AL530080
                                841 bp
                                        mRNA
                                               linear
                                                       EST 23-MAY-2003
DEFINITION AL530080 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
          cDNA clone CS0DD009YM06 3-PRIME, mRNA sequence.
ACCESSION
          AL530080
          AL530080.2 GI:31067915
VERSION
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
          1 (bases 1 to 841)
 AUTHORS
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
          Unpublished
COMMENT
          On Feb 13, 2001 this sequence version replaced gi:12793573.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
          was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
          9160.r For more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0DD009BG03NP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DD009BG03NP1.
FEATURES
                  Location/Qualifiers
    source
                  1. .841
                  /organism="Homo sapiens"
                  /mol type="mRNA"
```

```
/db xref="taxon:9606"
                /clone="CS0DD009YM06"
                /tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
                /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
            150 a
                   240 c
                          283 g
                                153 t
                                        15 others
ORIGIN
 Query Match
                   43.5%;
                         Score 520.2; DB 9; Length 841;
 Best Local Similarity
                   84.0%; Pred. No. 5.3e-108;
 Matches 647; Conservative
                         7; Mismatches
                                      86;
                                         Indels
                                                30; Gaps
Qy
       428 CGGTGCCGGAACCTGTATTGCTCT-CTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTA 486
           841 CGGTACCTGMACCCTTGTTGYTCTCCCCGGGCAGAGCTGCTTCTGCTAAGGCTCAAGTTA 782
Db
Qу
       487 AAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTC 546
           781 AAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATWCCTGGCGATACCTC 722
Db
       547 AGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGA 606
Qу
           721 AGCAACCSGCSGCTGGCACCCAGCSACTCGCCAGAGTGGTTTTCTTTTGTTGTCACCGKA 662
Db
       607 GTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCAC 666
Qу
           Db
       661 GTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTAAGG--TTTCGCCTTAGCGCCNAC 604
Qу
       667 TCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGC 726
             Db
       603 GGCTCCTGTAACAGCAGGGATAACACACTGCAAGTGAACATCAACGGGTTAACTACCGGC 544
       727 CGCCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCC 786
Qу
           Db
       543 CGCCGAGGTGACCTGGCCACCATTCTTGGCATGAACCGGCCTTTCCTGCTTCTCATGGCC 484
       787 ACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGACTACAAGGAT 846
Qу
           Db
       483 ACCCCGCTGGAGAGGGCCCAGCTTCTGCAAAGCTCCCGGCACCGCCGA------ 436
Qу
       847 GACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGC 906
                    Db
       435 ------GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGC 388
       907 GTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCC 966
Qу
           Db
       387 GTGCGGCAGCTGTACATTAACTTCCGCAAGGACCTCGGCTGGGAGTGGATCCACGAGCCC 328
Qу
       967 AAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACT 1026
          Db
       327 AAGGGCTWCCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACG 268
       Qу
```

Db	267	CAGGACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCCTCGGCGGCGCCC 210
Qy	1087	TGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCC 1146
Db	209	TGC-GCGTGCCGCAGGCGCTGGAGCCCCTTCGTGTACTACGTGGGCCGCAAGCCC 151
Qy	1147	AAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTG 1196
Db	150	AAGGTGGGGCGCTGTCCAACATGGTCGTGCGCTCCTGCAAGGGCCGCTG 101

Search completed: October 28, 2003, 00:08:04 Job time : 2979.42 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

October 27, 2003, 19:11:58; Search time 33.2026 Seconds Run on:

(without alignments)

1902.657 Million cell updates/sec

US-10-017-372E-9 Title:

Perfect score: 2114

1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

1107863 segs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:*

21:

24:

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:* 4: /SIDS1/qcgdata/geneseq/geneseqp-embl/AA1983.DAT:* 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:* 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* 15: /SIDS1/qcqdata/geneseq/geneseqp-embl/AA1994.DAT:* 16: /SIDS1/qcqdata/geneseq/geneseqp-emb1/AA1995.DAT:* 17: /SIDS1/qcqdata/geneseq/geneseqp-embl/AA1996.DAT:* 18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:* 19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:* 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*

/SIDS1/gcqdata/geneseg/genesegp-emb1/AA2000.DAT:* 22: /SIDS1/qcqdata/qeneseq/qeneseqp-emb1/AA2001.DAT:* 23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

1: /SIDS1/qcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•			50,	
		ક				
Result	0	Query	T	D D	TD	
No.	Score	Match	Length	DR	ID	Description
1	2053	97.1	390	23	AAE13596	Porcine transformi
2	1931	91.3	390	22	AAM39186	Human polypeptide
3	1924	91.0	390	7	AAP61468	PreTGF-beta gene p
4	1924	91.0	390	11	AAR04034	Sequence of pre-TG
5	1924	91.0	390	11	AAR05258	Human pre-transfor
6	1924	91.0	390	12	AAR13813	Human pro-TGF-beta
7	1924	91.0	390	16	AAR73596	Human TGF-beta 1 p
8	1924	91.0	390	17	AAR90827	Pre-transforming g
9	1921	90.9	390	23	AAU77101	Human transforming
10	1921	90.9	390	23	AAE16943	Human transforming
11	1920.5	90.8	391	24	ABB82780	TGFB1 Arg25Pro pol
12	1919	90.8	390	13	AAR20124	Sequence of simian
13	1915	90.6	390	15	AAR46227	Human pre-TGF-beta
14	1913.5	90.5	391	16	AAR83054	Transforming growt
15	1913	90.5	390	19	AAW78785	Human pre-transfor
16	1912	90.4	390	22	AAB84601	Nucleotide sequenc
17	1909.5	90.3	391	9	AAP81362	Human transforming
18	1908.5	90.3	434	11	AAR03743	Monkey transformin
19	1905	90.1	390	24	ABB82781	TGFB1 Arg25Pro pol
20	1888	89.3	386	11	AAR05663	Simian Transformin
21	1882.5	89.0	387	11	AAR05664	Simian Transformin
22	1872	88.6	390	11	AAR05492	Chimeric simian TG
23	1868	88.4	390	13	AAR27522	TGF-beta 1/beta 2
24	1848.5	87.4	389	13	AAR29657	TGF-beta 1. Homo
25	1843.5	87.2	453	22	AAM40972	Human polypeptide
26	1763	83.4	390	13	AAR20126	Sequence of hybrid
27	1762	83.3	390	11	AAR05749	Human TGF-Beta2 ex
28	1756	83.1	390	11	AAR05665	Human Transforming
29	1754	83.0	390	11	AAR05666	Hybrid transformin
30	1746.5	82.6	391	10	AAP91900	Sequence encoded b
31	1718.5	81.3	389	16	AAR79921	Simian-human hybri
32	1300	61.5	278	15	AAR53090	Polypeptide cross-
33	1295	61.3	278	12	AAR12541	Latency associated
34	1262.5	59.7	458	23	ABG31507	LAP-mIFNB construc
35	1262.5	59.7	463	23	ABG31510	LAP-huIFNB constru
36	1173.5	55.5	290	22	ABG06792	Novel human diagno
37	1135	53.7	450	23	ABG31508	mIFNB-LAP construc
38	1118	52.9	448	23	ABG31509	huIFNB-LAP constru
39	944	44.7	227	22	ABG20234	Novel human diagno
40	902.5	42.7	236	22	ABG20233	Novel human diagno
41	873	41.3	382	21	AAB08338	Amino acid sequenc
42	873	41.3	382	23	AAU77105	Frog transforming
43	837	39.6	456	19	AAW78786	Pig transforming g
44	836	39.5	412	16	AAR73598	Human TGF-beta 3 p
45	832	39.4	412	13	AAR20621	Transforming Growt

```
RESULT 1
AAE13596
ID
    AAE13596 standard; Protein; 390 AA.
XX
AC
    AAE13596;
XX
DТ
     26-FEB-2002 (first entry)
XX
DE
     Porcine transforming growth factor beta 1 (TGF-beta1) mutant.
XX
KW
     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW
     diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;
KW
     mutein.
XX
OS
     Sus scrofa.
XX
FΗ
     Key
                     Location/Qualifiers
FT
     Misc-difference 223
FT
                     /note= "Wild type Cys substituted with Ser"
FT
     Misc-difference 225
FT
                     /note= "Wild type Cys substituted with Ser"
XX
    WO200181404-A2.
PN
XX
PD
     01-NOV-2001.
XX
     20-APR-2001; 2001WO-US12980.
PF
XX
PR
     20-APR-2000; 2000US-199014P.
XX
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
ХX
ΡI
     Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
DR
    WPI: 2002-026155/03.
DR
     N-PSDB; AAD22696.
XX
PT
     Composition for treating autoimmune diseases e.g. inflammatory bowel
PT
     disease in humans, comprises vector containing transforming growth
PT
     factor-beta under the control of inducible promoter -
XX
₽S
     Example 1; Fig 1; 78pp; English.
XX
CC
     The invention relates to a composition containing a vector comprising a
CC
     gene encoding a regulatory transcription factor under the control of a
CC
     promoter encoding a transforming growth factor-beta (TGF-beta). The
     vector is useful for expressing TGF-beta, such as TGF-betal, TGF-beta2
CC
     or TGF-beta3, its variants or homologues, by transfecting a cell which
CC
CC
     is part of a host suspected of having an autoimmune disease, especially
CC
     inflammatory bowel disease (IBD), under conditions such that the
CC
    polypeptide encoded by the nucleic acid sequence in the vector is
     expressed. The vector is delivered using a delivery system. The delivery
CC
CC
     of the vector results in substantial elimination of symptoms of the
CC
     autoimmune disease and increased production of IL-10 by the host. The
CC
     composition is useful for treating various diseases with an autoimmune
```

```
CC
    component such as multiple sclerosis, rheumatoid arthritis, systemic
CC
    lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC
    and psoriasis, and also for assaying the expression of a gene in a cell.
CC
    The vector is further useful for screening of the effect of test
CC
    compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC
    The present sequence is porcine TGF-betal mutant.
XX
SO
    Sequence
             390 AA;
                      97.1%; Score 2053; DB 23; Length 390;
 Query Match
 Best Local Similarity
                      98.0%; Pred. No. 1.3e-174;
 Matches 390; Conservative
                            0; Mismatches
                                           0;
                                              Indels
                                                       8; Gaps
                                                                 1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            Db
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
            Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            1111111111
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
Db
RESULT 2
AAM39186
ID
    AAM39186 standard; Protein; 390 AA.
XX
AC
    AAM39186;
XX
DT
    22-OCT-2001 (first entry)
XX
DE
    Human polypeptide SEQ ID NO 2331.
XX
KW
    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
    peripheral nervous system; neuropathy; central nervous system; CNS;
KW
KW
    Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW
    amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
    chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW
```

```
KW
     leukaemia.
XX
OS
     Homo sapiens.
XX
PN
     WO200153312-A1.
XX
PD
     26-JUL-2001.
XX
PF
     26-DEC-2000; 2000WO-US34263.
XX
PR
     21-JAN-2000; 2000US-0488725.
PR
     25-APR-2000; 2000US-0552317.
PR
     09-JUL-2000; 2000US-0598042.
     19-JUL-2000; 2000US-0620312.
PR
PR
     03-AUG-2000; 2000US-0653450.
PR
     14-SEP-2000; 2000US-0662191.
PR
     19-OCT-2000; 2000US-0693036.
PR
     29-NOV-2000; 2000US-0727344.
XX
PΑ
     (HYSE-) HYSEQ INC.
XX
     Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y,
PΙ
                                                              Ren F, Wang D;
PΙ
                                                              Zhang J;
ΡI
     Zhao OA, Zhou P, Goodrich R, Drmanac RT;
XX
DR
     WPI; 2001-442253/47.
DR
     N-PSDB; AAI58342.
XX
PT
     Novel nucleic acids and polypeptides, useful for treating disorders
PT
     such as central nervous system injuries -
XX
PS
     Example 4; SEQ ID NO 2331; 10078pp; English.
XX
CC
     The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC
     the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC
     immunosuppressant and cytostatic activity. The polynucleotides are useful
CC
     in gene therapy. A composition containing a polypeptide or polynucleotide
CC
     of the invention may be used to treat diseases of the peripheral nervous
CC
     system, such as peripheral nervous injuries, peripheral neuropathy and
CC
     localised neuropathies and central nervous system diseases, such as
CC
     Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC
     lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC
     utilisation of the activities such as: Immune system suppression,
CC
     Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC
     and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC
     assays for receptor activity, arthritis and inflammation, leukaemias and
CC
     C.N.S disorders.
CC
     Note: The sequence data for this patent did not form part of the printed
CC
     specification.
XX
SQ
     Sequence
                390 AA;
  Query Match
                           91.3%; Score 1931; DB 22; Length 390;
                          92.0%; Pred. No. 1e-163;
 Best Local Similarity
 Matches 366; Conservative 10; Mismatches
                                                   14;
                                                         Indels
```

Оy

```
1 MPPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
           61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYQKYSNDSWR 180
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qy
           11111111111111
                                     181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR----
Db
                                               --ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qy
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qy
           353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 3
AAP61468
ID
    AAP61468 standard; Protein; 390 AA.
XX
AC
   AAP61468;
XX
DT
    31-OCT-2002
              (updated)
DT
    28-OCT-1991
              (first entry)
XX
DE
    PreTGF-beta gene product.
XX
KW
    Transforming growth factor beta; cancer; wound healing.
XX
OS
    Unidentified.
XX
FH
    Key
                Location/Qualifiers
FT
    Protein
                279..390
XX
PN
    EP200341-A.
XX
PD
    10-DEC-1986.
XX
PF
    21-MAR-1986;
                86EP-0302112.
XX
PR
    22-MAR-1985;
               85US-0715142.
PR
    13-MAR-1987;
               87US-0025423.
XX
    (GETH ) GENENTECH INC.
PA
XX
```

```
PΙ
   Derynck RMA;
XX
DR
    WPI; 1986-326875/50.
DR
    N-PSDB: AAN60972.
XX
PT
    TGF-beta prodn. from transformed hosts - useful esp. for treating
PT
    wounds (J6 2/9/86).
XX
PS
    Disclosure; Fig 1b; 26pp; English.
XX
CC
    The gene product is known to stimulate cell proliferation and
CC
    inhibit anchorage-dependent growth of a variety of human cancer cell
    lines, it is esp. useful in treatment of burns and the promotion of
CC
CC
    surface and internal wound healing. TGF-beta may be expressed from a
    transformed CHO cell line.
CC
CC
    (Updated on 31-OCT-2002 to add missing OS field.)
XX
SO
    Sequence
             390 AA;
 Query Match
                     91.0%; Score 1924; DB 7; Length 390;
 Best Local Similarity
                     91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                     8; Gaps
                                                               1;
Qу
          1 MAPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
           1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
QУ
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEOHVELYOKYSNDSWR 180
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNNSWR 180
Dh
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 4
   AAR04034 standard; protein; 390 AA.
ID
XX
AC
   AAR04034;
```

```
XX
DT
     25-MAR-2003
                 (updated)
DT
     31-OCT-2002
                 (updated)
DT
     31-MAY-1989 (first entry)
XX
DE
    Sequence of pre-TGF-beta 1.
XX
KW
     Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW
     inhibition.
XX
OS
    Homo sapiens.
XX
                   Location/Oualifiers
FΗ
     Key
FT
    CDS
                   348..500
XX
PN
    WO8912101-A.
XX
PD
    14-DEC-1989.
XX
PF
     08-JUN-1988;
                  88WO-US01945.
XX
PR
    08-JUN-1988;
                  88WO-US01945.
XX
PΑ
     (GETH ) GENENTECH INC.
XX
PΙ
    Dernyck RMA, Goeddel DV;
XX
DR
    WPI: 1990-007474/01.
DR
    N-PSDB; AAQ02815.
XX
PT
    Nucleotide sequence encoding transforming growth factor beta-3 used as a
    probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT
PT
    and neoplastic cells, eg A549.
XX
PS
    Disclosure; Fig. 2; 61pp; English.
XX
CC
    Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta
CC
    1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The
CC
    nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful
CC
    as a probe or to produce TGF-beta 3 for inhibition of normal and
    neoplastic cell growth.
CC
CC
     (Updated on 31-OCT-2002 to add missing OS field.)
     (Updated on 25-MAR-2003 to correct PR field.)
CC
CC
     (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ
    Sequence
               390 AA;
  Query Match
                        91.0%; Score 1924; DB 11; Length 390;
 Best Local Similarity
                        91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches
                                                             8; Gaps
                                               15; Indels
Qу
           1 MAPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
             Db
           1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
```

```
Db
         61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
            Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QУ
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 5
AAR05258
ID
    AAR05258 standard; protein; 390 AA.
XX
AC
    AAR05258;
XX
DT
    25-MAR-2003 (updated)
DT
    05-AUG-1990 (first entry)
XX
DE
    Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
XX
KW
    Transforming growth factor-beta-1 (TGF-beta-1);
KW
    neoplastic cell line inhibition;
KW
    EGF-potentiated anchorage-independent growth.
XX
OS
    Homo sapiens.
XX
FH
    Key
                  Location/Qualifiers
FT
    Peptide
                  1..278
    Protein
FT
                  279..2011
FT
    Domain
                  8..23
FT
                  /note="hydrophobic domain"
FT
    Modified-site
                  82..84
FT
                  /note="potential N-glycosylation site "
FT
    Modified-site
                  136..138
                  /note="as above"
FT
FT
                  176..178
    Modified-site
                  /note="as above"
FT
FT
    Cleavage-site
                  277..278
FT
                  /note="proteolytic cleavage site"
XX
    US4886747-A.
PN
XX
PD
    12-DEC-1989.
```

```
XX
ΡF
    13-MAR-1987;
                 87US-0025423.
XX
PR
                87US-0025423.
    13-MAR-1987;
PR
    22-MAR-1985;
                85US-0715142.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynck RMA, Goeddel DV;
XX
    WPI; 1990-051338/07.
DR
DR
    N-PSDB; AAQ93301.
XX
PT
    Nucleic acid encoding transforming growth factor-beta -
    cloned into expression vectors for expression in eukaryotic host
PT
PT
    cells for therapeutic use
XX
PS
    Disclosure; Fig 1b; 28pp; English.
XX
CC
    Pre-TGF-beta-1 is a polypeptide of 390 amino acids. Post-transitional
CC
    cleavage of the precursor gives rise to the mature TGF-beta monomer.
CC
    The sequence for human TGF-beta was determined by direct amino acid
CC
    sequence analysis and by deduction from the TGF-beta cDNA. It is
CC
    capable of inducing EGF-potentiated anchorage-independent growth of
    target cell lines, and/or growth inhibition of neoplastic cell lines.
CC
CC
    can be used for treating wounds, eg burns or epidermal ulcers.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
    Sequence
             390 AA;
 Query Match
                      91.0%; Score 1924; DB 11; Length 390;
 Best Local Similarity
                      91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches
                                          15; Indels
                                                       8; Gaps
                                                                  1;
          1 MAPSGLRLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
ďŪ
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFSSTEKN 292
Db
Qу
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 360
            Dh
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
```

```
Qу
         361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
              353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 6
AAR13813
    AAR13813 standard; Protein; 390 AA.
ID
XX
AC
    AAR13813;
XX
DT
    20-NOV-1991 (first entry)
XX
    Human pro-TGF-beta 1.
DE
XX
KW
    Osteogenetic; tumoricidal.
XX
OS
    Homo sapiens.
XX
FΗ
                    Location/Qualifiers
     Key
FT
     Peptide
                    1..29
FT
                    /note= "signal peptide"
FT
                    30..390
     Peptide
FT
                    /note= "pro-TGF-beta 1"
FT
     Peptide
                    279..390
FT
                    /note= "TGF-beta 1"
XX
PN
    JP03180192-A.
XX
PD
     06-AUG-1991.
XX
ΡF
     07-DEC-1989;
                   89JP-0318243.
XX
PR
     07-DEC-1989;
                   89JP-0318243.
XX
Aq
     (KIRI ) KIRIN BREWERY KK.
XX
DR
    WPI; 1991-271579/37.
DR
    N-PSDB; AAQ13392.
XX
PT
     Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT
     preparing DNA chain contg. base sequence coding for human
PT
     pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS
     Claim 1; Fig 1; 16pp; Japanese.
XX
     The amino acid sequence codes for human prepro-TGF-beta 1 which
CC
     can be produced by recombinant methods, it has osteogenetic and
CC
CC
     tumoricidal activity.
XX
               390 AA;
SO
    Sequence
                         91.0%; Score 1924; DB 12;
  Query Match
                                                      Length 390;
                         91.7%; Pred. No. 4.4e-163;
  Best Local Similarity
  Matches 365; Conservative 10; Mismatches 15; Indels
                                                                8; Gaps
                                                                            1;
```

```
1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           Db
         1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
QУ
           61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           Db
        121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 7
AAR73596
TD
    AAR73596 standard; Protein; 390 AA.
XX
AC
    AAR73596;
XX
DT
    25-MAR-2003
              (updated)
DT
    20-DEC-1995
              (first entry)
XX
DE
    Human TGF-beta 1 protein.
XX
KW
    Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;
KW
    TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
    bone-inducing cofactor.
KW
XX
OS
    Homo sapiens.
XX
PN
    US5409896-A.
XX
PD
    25-APR-1995.
XX
PF
    12-NOV-1993;
                93US-0132405.
XX
PR
    01-SEP-1989:
                89US-0401906.
                91US-0790856.
PR
    12-NOV-1991;
PR
    18-MAY-1993;
                93US-0063841.
PR
    12-NOV-1993;
                93US-0132405.
XX
```

```
(GETH ) GENENTECH INC.
PA
XX
PΙ
    Ammann AJ, Rudman CG;
XX
DR
    WPI; 1995-169610/22.
XX
PT
    Compsn. for treating skeletal tissue deficiency - comprising
PT
    transforming growth factor-beta and an osteogenic cell source in a
PT
    carrier
XX
PS
    Claim 3; Column 15-18; 19pp; English.
XX
CC
    This sequence represents human transforming growth factor-beta 1
CC
    (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see
CC
    AAR73598) are claimed within the scope of the invention. The invention
CC
    is a composition consisting of a TGF-beta protein and an osteogenic cell
CC
    source (OCS) formulated in an acceptable carrier other than a bone
CC
    morphogenic cofactor. This composition can be used for the restoration
CC
    of bone deficiency. This provides for the generation of mature bone
    only where it is required, without the inclusion of a specific
CC
CC
    bone-inducing cofactor. This method can be used with any of the 5 human
CC
    TGF-beta's or with TGF-beta from other species.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence 390 AA;
 Query Match
                      91.0%; Score 1924; DB 16; Length 390;
 Best Local Similarity
                      91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
                                                       8; Gaps
                                                                 1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Dh
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Db
QУ
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 360
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
```

```
RESULT 8
AAR90827
     AAR90827 standard; Protein; 390 AA.
ΙD
XX
     AAR90827;
AC
XX
                  (updated)
DT
     25-MAR-2003
                  (first entry)
DT
     25-JAN-1980
XX
DE
     Pre-transforming growth factor beta 1.
XX
     transforming growth factor beta 1; wound healing;
KW
KW
     recombinant production.
XX
OS
     Homo sapiens.
XX
FΗ
                     Location/Qualifiers
     Key
FT
     Domain
                      8..23
FT
                      /note= "hydrophobic domain"
FT
     Modified-site
                      82..84
FT
                      /note= "potential N-glycosylation site"
     Modified-site
FT
                      136..138
                      /note= "potential N-glycosylation site"
FT
FT
     Modified-site
                      176..178
FT
                      /note= "potential N-glycosylation site"
FT
     Cleavage-site
                     277..279
FT
                      /note= "trypsin-like peptidase cleavage site"
FT
     Protein
                      279..390
FT
                      /label= mature TGF beta 1
XX
PN
     US5482851-A.
XX
PD
     09-JAN-1996.
XX
ΡF
     05-NOV-1993;
                    93US-0147364.
XX
PR
     13-MAR-1987;
                    87US-0025423.
     22-MAR-1985;
                    85US-0715142.
PR
     04-AUG-1989;
                    89US-0389929.
PR
                    92US-0845893.
PR
     04-MAR-1992;
PR
     05-NOV-1993;
                    93US-0147364.
XX
PA
     (GETH ) GENENTECH INC.
XX
     Derynck RMA, Goeddel DV;
ΡI
XX
DR
     WPI; 1996-076891/08.
     N-PSDB; AAT15720.
DR
XX
     New recombinant human transforming growth factor-beta prods. - produced
PT
     using Chinese hamster ovary cells, for use in diagnostic applications
PT
     or in therapy
PT
XX
     Example 3; Fig 1A-C; 26pp; English.
PS
XX
```

```
CC
    by AAT15720. The mature TGF beta 1 monomer is cleaved from the
CC
    precursor at the Arg-Arg dipeptide immediately preceding the mature
CC
    TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal
CC
    signal peptide typical of most secreted proteins. The pre-TGF beta 1
CC
    contains several pairs of basic residues which could undergo
CC
    post-translational cleavage and give rise to separate polypeptide
    entities. The precursor contains 3 potential N-glycosylation sites, none
CC
    of which are localised in the mature TGF beta 1. This is useful in
CC
CC
    purification of the mature protein. TGF beta 1 can be used in, e.g. wound
CC
    healing.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence
             390 AA;
 Query Match
                      91.0%; Score 1924; DB 17; Length 390;
 Best Local Similarity
                     91.7%; Pred. No. 4.4e-163;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                      8; Gaps
                                                                1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            1 MPPSGLRLLPLLUPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Oy
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLKVEOHVELYOKYSNDSWR 180
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
            Dh
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
AAU77101
    AAU77101 standard; Protein; 390 AA.
ID
XX
AC
    AAU77101:
XX
DT
    05-JUN-2002 (first entry)
XX
    Human transforming growth factor beta 1 (TFG-beta-1) polypeptide.
DE
```

The pre-transforming growth factor (TGF) beta 1 protein is encoded

CC

```
XX
KW
     Human; transforming growth factor beta; TGF-beta; insulin production;
KW
     type I diabetes mellitus; pancreatic cell outgrowth; wound healing;
KW
     pancreatic duct tissue; ischaemia; stroke; nervous system aging;
     neurological condition; neurodegenerative disease; inflammation;
KW
KW
     vasal injury; chemical injury; traumatic injury; tumour-induced injury;
KW
     amyotrophic lateral sclerosis; spinocerebellar degeneration;
KW
     immunological disease; multiple sclerosis; TGF-beta-1.
XX
OS
     Homo sapiens.
XX
PN
     WO200212336-A2.
XX
PD
     14-FEB-2002.
XX
PF
     09-FEB-2001; 2001WO-US04192.
XX
PR
     09-AUG-2000; 2000US-0635368.
XX
PA
     (CURI-) CURIS INC.
XX
PΙ
     Wang M, Pang K;
XX
DR
     WPI; 2002-257468/30.
XX
PT
     Treating a subject with a disorder resulting from insufficient insulin
PT
     production, and inducing outgrowth of pancreatic cells, involves using
PT
     a transforming growth factor beta therapeutic -
XX
PS
     Disclosure; Fig 1; 77pp; English.
XX
CC
     The invention relates to treating a subject with a disorder resulting
CC
     from insufficient insulin production, involving contacting the subject
CC
     with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta
CC
     polypeptides can be used for treating a subject with a disorder resulting
     from insufficient insulin production, e.g. type I diabetes mellitus, and
CC
CC
     for inducing outgrowth of pancreatic cells associated with pancreatic
CC
     duct tissue within a subject. A composition comprising a TGF-beta protein
CC
     may be useful in wound healing and treatment of neurological conditions
CC
     derived from acute, subacute or chronic injury to the nervous system,
CC
     including traumatic injury, chemical injury, vasal injury and deficits
CC
     (such as ischaemia resulting from stroke), together with
CC
     infectious/inflammatory and tumour-induced injury, aging of the nervous
     system including Alzheimer's disease, chronic neurodegenerative diseases
CC
CC
     including Parkinson's disease, Huntington's chorea, amyotrophic lateral
CC
     sclerosis, spinocerebellar degenerations and chronic immunological
CC
     diseases of the nervous system or affecting the nervous system, including
CC
     multiple sclerosis. This sequence represents the human TGF-beta-1
CC
     protein.
XX
SO
     Sequence
                390 AA;
  Query Match
                          90.9%; Score 1921; DB 23; Length 390;
                          91.7%; Pred. No. 8.1e-163;
 Best Local Similarity
 Matches 365; Conservative 10; Mismatches
                                                  15;
                                                      Indels
                                                                              1;
```

QУ

```
1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
           SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----
                                                --ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 10
AAE16943
ID
    AAE16943 standard; Protein; 390 AA.
XX
AC
    AAE16943;
XX
DT
    18-APR-2002 (first entry)
XX
DE
    Human transforming growth factor-betal (TGF-betal) protein.
XX
KW
    Human; transforming growth factor-betal; TGF-betal; osteoporosis;
    latency associated peptide; LAP; integrin alphavbeta3; apoptosis;
KW
    immunomodulation; inflammatory disease; fibrotic disease; cancer;
KW
KW
    diabetic retinopathy; chronic obstructive pulmonary disorder;
KW
    bone resorption; rheumatoid arthritis; psoriasis; restenosis;
KW
    atherosclerosis; liver fibrosis; asthma; cytostatic; osteopathic;
    ophthalmological; antiarteriosclerotic; vasotropic.
KW
XX
OS
    Homo sapiens.
XX
FH
    кеу
                 Location/Qualifiers
FT
    Peptide
                 1..29
FT
                 /label= Signal peptide
FT
    Region
                 30..278
                 /note= "LAP-beta1"
FT
FT
    Domain
                 244..246
FT
                 /note= "RGD motif"
                 279..390
FT
    Protein
FT
                 /note= "Human mature TGF-betal protein"
```

```
XX
ΡN
    WO200190186-A1.
XX
PD
    29-NOV-2001.
XX
    25-MAY-2001; 2001WO-GB02352.
PF
XX
    26-MAY-2000; 2000GB-0012991.
PR
    05-JAN-2001; 2001GB-0000286.
PR
XX
     (GLAX ) GLAXO GROUP LTD.
PA
XX
    Ludbrook S, Barry S, Horgan C, Miller D;
PΙ
XX
DR
    WPI; 2002-097645/13.
XX
    Identifying modulators of interactions between latency associated
PT
    peptides and integrin alphavbeta3 for therapeutics, by contacting the
PT
    peptide and integrin with a test product and determining if the product
PT
PT
    modulates interaction -
XX
PS
    Disclosure; Page 37-39; 44pp; English.
XX
    The invention relates to a method for identification of a modulator
CC
    of the interaction between latency associated peptide (LAP) of
CC
CC
    transforming growth factor-betal (TGF-betal) and integrin alphavbeta3.
    The method is useful for identifying a modulator of the interaction
CC
CC
    between LAP and integrin alphavbeta3. The method is useful for
CC
    immunomodulation, in the treatment of inflammatory disease, fibrotic
CC
    disease, cancer, diabetic retinopathy, bone resorption or osteoporosis,
CC
    and for preventing apoptosis administering the modulator to the host.
CC
    The modulator (inhibitor of the interaction between LAP-betal and
CC
    integrin alphavbeta3) is useful in the manufacture of a medicament for
CC
    immunomodulation. The modulator (activator of the interaction between
CC
    LAP-betal and integrin alphavbeta3 ) is useful in the manufacture of
CC
    medicament for preventing apoptosis. The modulator is useful for
CC
    treating a inflammatory or fibrotic disease such as chronic obstructive
CC
    pulmonary disorder, rheumatoid arthritis, psoriasis, restenosis,
CC
    atherosclerosis, liver fibrosis and asthma. The present sequence is
CC
    human TGF-betal protein.
XX
SQ
    Sequence
               390 AA;
  Ouery Match
                        90.9%; Score 1921; DB 23; Length 390;
 Best Local Similarity 91.7%; Pred. No. 8.1e-163;
 Matches 365; Conservative 10; Mismatches
                                              15;
                                                  Indels
QУ
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
             Db
           1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
             61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
```

```
Db
         121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QУ
             181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
QУ
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
             11111111111
Dh
         241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 360
Qу
             Db
         293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
         361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
             Db
         353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 11
ABB82780
ID
    ABB82780 standard; Protein; 391 AA.
XX
AC
    ABB82780;
XX
DT
    18-MAR-2003 (first entry)
XX
DE
    TGFB1 Arg25Pro polymorphism G-allele protein sequence.
XX
KW
    Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;
KW
    renal failure; nephrotropic; human; allele.
XX
OS
    Homo sapiens.
XX
PN
    WO200290585-A2.
XX
PD
    14-NOV-2002.
XX
PF
    08-MAY-2002; 2002WO-GB02066.
XX
PR
    09-MAY-2001; 2001GB-0011277.
XX
PA
    (UYSH-) UNIV SHEFFIELD HALLAM.
XX
ΡI
    El-Nahas AM, Blakemore A, Khalil MS;
XX
DR
    WPI; 2003-120560/11.
    N-PSDB; ABV75391.
DR
XX
PT
    Determining an individual's susceptibility to the progression of renal
PT
    failure comprises detecting the presence of a genetic polymorphism
    pattern in transforming growth factor beta 1 (TGFB1) gene in a sample
PT
PT
    from the individual
XX
PS
    Claim 51; Page 59-61; 62pp; English.
XX
    The invention relates to determining an individual's susceptibility to
CC
```

```
renal failure and invovles detecting the presence of a genetic
CC
    polymorphism pattern in transforming growth factor beta 1 (TGFB1) gene in
CC
    a sample from an individual, where polymorphism pattern is associated
CC
    with renal failure. The method is useful for determining an individual's
CC
    susceptibility to the progression of renal failure. The nucleic acid
CC
    comprising a T(-509)C polymorphism of TGFB1 gene, or a polypeptide
CC
    comprising a sequence of 391 amino acids is useful for preparing a
CC
    medicament for retarding or preventing the progression of renal disease,
CC
    and for drug research purposes for retarding or preventing the
CC
    progression of renal disease. Sequences ABV75386-88 represents the
CC
    protein sequence for the TGFB1 G-allele of the Arg25Pro polymorphism
CC
    of exon 1.
XX
SO
    Sequence
             391 AA;
                      90.8%; Score 1920.5; DB 24; Length 391;
 Query Match
 Best Local Similarity
                      91.7%; Pred. No. 9e-163;
 Matches 366; Conservative 10; Mismatches 14; Indels
                                                       9; Gaps
                                                                 2;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEOHVELYOKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
            181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Dh
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
             241 TTGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEK 292
Db
        300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
Qу
            293 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 352
Db
        360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
QУ
            Db
        353 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
RESULT 12
ID
    AAR20124 standard; Protein; 390 AA.
XX
AC
   AAR20124;
XX
DT
    25-MAR-2003
               (updated)
               (first entry)
DT
    16-APR-1992
XX
```

CC

```
XX
KW
    Hypertension therapy; hypotensive agent; blood pressure modulator.
XX
OS
    Monkey.
XX
FΗ
    Key
                   Location/Qualifiers
FT
    Peptide
                   8..21
FT
    Protein
                   279..390
XX
PN
    WO9119513-A.
XX
PD
    26-DEC-1991.
XX
PF
    20-JUN-1991;
                91WO-US04449.
XX
PR
    20-JUN-1990;
                90US-0541221.
XX
PA
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PΙ
    Oleson FB, Comereski CR;
XX
DR
    WPI; 1992-024199/03.
DR
    N-PSDB; AAQ20289.
XX
    Use of transforming growth factor (TGF)-beta and their
PT
PT
    antagonists - for modulating blood pressure, for treating
PT
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CC
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
    Sequence
              390 AA;
 Query Match
                       90.8%; Score 1919; DB 13; Length 390;
 Best Local Similarity 91.5%; Pred. No. 1.2e-162;
 Matches 364; Conservative 10; Mismatches 16; Indels
                                                           8; Gaps
                                                                      1;
QУ
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
             1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGOILSKLRLA 60
dG
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
             Db
          61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
             Db
         121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
```

Sequence of simian transforming growth factor (TGF) beta-1.

DE

```
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qy
            Db
        353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 13
AAR46227
    AAR46227 standard; Protein; 390 AA.
XX
AC
    AAR46227;
XX
DT
    25-MAR-2003 (updated)
DT
    09-JUL-1994 (first entry)
XX
DE
    Human pre-TGF-beta-1.
XX
KW
    TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW
    transforming growth factor beta-3; recombinant; wound healing;
KW
    vulnerary.
XX
OS
    Homo sapiens.
XX
FH
                  Location/Qualifiers
    Key
FT
    Peptide
                  279..390
FT
                  /label = Mat peptide
FT
    Cleavage-site
                  279
FT
                  /note= "TGF-beta-1 release site"
FΤ
    Modified-site
                  82..84
FT
                  /label= N-glycosylation_site
FT
    Modified-site
                  136..138
                  /label= N-glycosylation site
FT
FT
    Modified-site
                  176..178
FT
                  /label= N-glycosylation site
XX
PN
    US5284763-A.
XX
PD
    08-FEB-1994.
XX
PF
    04-MAR-1992;
                92US-0845893.
XX
PR
    22-MAR-1985;
                 85US-0715142.
PR
    13-MAR-1987;
                 87US-0025423.
PR
    04-AUG-1989;
                 89US-0389929.
PR
    04-MAR-1992;
                 92US-0845893.
```

```
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynk RMA, Goeddel DV;
XX
DR
    WPI; 1994-056343/07.
DR
    N-PSDB; AAQ56923.
XX
PT
    Nucleic acid sequences encoding transforming growth factor-beta -
PT
    diagnostic probes, and for use in therapeutics
XX
PS
    Disclosure; Fig 1b; 25pp; English.
XX
CC
    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC
    pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC
    corresponding amino acid sequences were determined (AAR46227-29,
CC
    respectively). A genomic fragment corresponding to a human TGF-
CC
    beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC
    determined (AAR46230). The sequences have been used in the
CC
    construction of vectors for the expression of recombinant TGF-
CC
    beta.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence
             390 AA;
 Query Match
                      90.6%; Score 1915; DB 15; Length 390;
 Best Local Similarity 91.5%; Pred. No. 2.8e-162;
 Matches 364; Conservative 10; Mismatches
                                          16: Indels
                                                       8; Gaps
                                                                 ٦.
Qу
          1 MAPSGLRLLPLLLVLLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEREPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                       Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLSRGGEIEGFRLSAHCSCDSRDNTLOVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
            111111111111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
```

```
RESULT 14
AAR83054
     AAR83054 standard; Protein; 391 AA.
XX
AC
     AAR83054;
XX
DT
     25-JUN-1996 (first entry)
XX
DE
     Transforming growth factor-beta 1.
XX
KW
     macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW
     interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW
     nitric oxide production; hypotension; inflammation; septic shock;
KW
     treatment.
XX
OS
     Mammalian sp.
XX
FΗ
                     Location/Qualifiers
     Key
FT
     Protein
                     279..391
FT
                     /note= "represents the mature active TGF beta-1 mol."
XX
NQ
     WO9526745-A1.
XX
PD
     12-OCT-1995.
XX
PF
     05-APR-1994;
                    94WO-US03705.
XX
PR
     05-APR-1994;
                   94WO-US03705.
XX
PA
     (HARD ) HARVARD COLLEGE.
XX
     Lee M, Perrella MA;
PΙ
XX
DR
     WPI; 1995-358443/46.
     N-PSDB; AAT05876.
DR
XX
PT
     Treatment of hypotension, esp. in septic shock - by administering
PT
     transforming growth factor-beta e.g. to inhibit inducible nitric
PT
     oxide synthase gene transcription
XX
PS
     Disclosure; Fig 17; 52pp; English.
XX
CC
     Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit
CC
     inducible nitric oxide synthase (iNOS) gene transcription, esp. in
CC
     interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at
CC
     a dose which does not inhibit consitutive NOS. TGF-beta 1 or 2
CC
     (AAR83055) or their active fragments (esp. derived from the
CC
     carboxy-terminal 112 amino acids), can be used in the treatment of
CC
     hypotension, such as that associated with severe inflammation or septic
CC
     shock.
XX
SO
     Sequence
                391 AA;
                          90.5%; Score 1913.5; DB 16; Length 391; 91.5%; Pred. No. 3.8e-162;
  Query Match
  Best Local Similarity
  Matches 365; Conservative 10; Mismatches
                                                   15; Indels
                                                                   9; Gaps
                                                                               2;
```

```
Qу
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
           Db
         1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Dh
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
           181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
            1111111111111
        241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEK 292
Db
        300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
Qу
           293 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 352
Db
        360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
Dh
RESULT 15
AAW78785
TD
    AAW78785 standard; Protein; 390 AA.
XX
AC
    AAW78785;
XX
DT
    25-MAR-2003
               (updated)
DT
    21-DEC-1998
              (first entry)
XX
DE
    Human pre-transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; TGF-beta 1; human.
XX
OS
    Homo sapiens.
XX
FH
    Key
                 Location/Qualifiers
FT
    Domain
                 8..23
                 /note= "hydrophobic domain"
FT
FT
                 279..390
    Protein
FT
                 /label= Mat protein
FT
    Modified-site
                 82..84
                 /note= "Asn is N-glycosylated"
FT
FT
    Modified-site
                 136..138
FT
                 /note= "Asn is N-glycosylated"
FT
    Modified-site
                 176..178
FT
                 /note= "Asn is N-glycosylated"
FT
                 277..278
    Cleavage-site
```

```
FT
                   /note= "cleavage site for relase of TGF-beta 1"
XX
PN
    US5801231-A.
XX
PD
    01-SEP-1998.
XX
PF
    30-MAY-1995; 95US-0454468.
XX
PR
    13-MAR-1987; 87US-0025423.
PR
    22-MAR-1985; 85US-0715142.
PR
    04-AUG-1989; 89US-0389929.
PR
    04-MAR-1992; 92US-0845893.
PR
    05-NOV-1993;
                  93US-0147364.
    30-MAY-1995;
PR
                95US-0454468.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynck RMA, Goeddel DV;
XX
DR
    WPI; 1998-494840/42.
    N-PSDB; AAV52933.
DR
XX
PT
    DNA encoding transforming growth factor-beta precursor sequence -
PT
    useful for analysis to perform manipulations to increase yield of
PT
    recombinant production of the protein
XX
PS
    Example 3; Fig 1B 1-3; 26pp; English.
XX
CC
    This is the amino acid sequence of human transforming growth
CC
    factor-beta 1 precursor (preTGF-beta 1). It was deduced from
CC
    a preTGF-beta 1 cDNA sequence (see AAV52933). The invention relates
CC
    to the recombinant production of TGF-beta. Biologically active
CC
    TGF-beta is defined as being capable of inducing EGF-potentiated
CC
    anchorage independent growth of target cell lines and/or growth
CC
    inhibition of neoplastic cell lines. Nucleic acids encoding
CC
    TGF-beta have been isolated and cloned into vectors which are
CC
    replicated in bacteria and expressed in eukaryotic cells. TGF-beta
CC
    recovered from transformed cells is used in known therapeutic
CC
    applications.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence
              390 AA;
 Query Match
                        90.5%; Score 1913; DB 19;
                                                  Length 390;
 Best Local Similarity
                       91.2%; Pred. No. 4.2e-162;
 Matches 363; Conservative 10; Mismatches
                                            17; Indels
                                                           8; Gaps
Qу
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
             Db
           1 MPPSGLRLLPLLLPLLWLLVLTPGPPAPGLSTCKTIDMEOVKRKRIEAIRGOILSKLRLA 60
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
             Db
          61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
QУ
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
```

Db	121	YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180						
Qy	181	LSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 24						
Db	181							
Qy	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300						
Db	241	:						
Qy	301	CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360						
Db	293	CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352						
Qy	361	APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398						
Db	353							
Search completed: October 28, 2003, 09:06:45 Job time: 36.2026 secs								
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.								
OM protein - protein search, using sw model								
Run on:		October 28, 2003, 09:09:54 ; Search time 24.1473 Seconds (without alignments) 2760.110 Million cell updates/sec						
Title:		US-10-017-372E-9						
Perfect score Sequence:		2114 1 MAPSGLRLLPLLLPLLWLLVGRKPKVEQLSNMIVRSCKCS 398						
Scoring table:		BLOSUM62 Gapop 10.0 , Gapext 0.5						
Searched:		629382 seqs, 167460630 residues						
Total number of hits satisfying chosen parameters: 629382								
Minimum DB seq length: 0 Maximum DB seq length: 2000000000								
Post-proce	essin	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries						
Database :		Published_Applications_AA:* 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:* 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*						

```
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ક			SOMMAKIES	
Result		Query				
No.	Score		Length	DB	ID	Description
1	2035	96.3	390	11	US-09-214-592-26	Sequence 26, Appl
2	1934	91.5	390	11	US-09-214-592-29	Sequence 29, Appl
3	1931	91.3	390	15	US-10-087-268-2	Sequence 2, Appli
4	1924	91.0	390	15	US-10-087-268-5	Sequence 5, Appli
5	1921	90.9	390	12	US-10-276-947-1	Sequence 1, Appli
6	1919	90.8	390	11	US-09-214-592-33	Sequence 33, Appl
7	1913.5	90.5	391	11	US-09-214-592-17	Sequence 17, Appl
8	1910	90.4	390	10	US-09-756-283A-23	Sequence 23, Appl
9	1898	89.8	390	11	US-09-214-592-28	Sequence 28, Appl
10	1840	87.0	390	11	US-09-214-592-20	Sequence 20, Appl
11	1840	87.0	390	11	US-09-214-592-23	Sequence 23, Appl
12	1577	74.6	315	11	US-09-214-592-25	Sequence 25, Appl
13	1262.5	59.7	455	10	US-09-756-283A-20	Sequence 20, Appl
14	1139	53.9	447	10	US-09-756-283A-22	Sequence 22, Appl
15	1059.5	50.1	373	11	US-09-214-592-32	Sequence 32, Appl
16	876	41.4	412	11	US-09-214-592-31	Sequence 31, Appl
17	873	41.3	382	11	US-09-214-592-34	Sequence 34, Appl
18	872.5	41.3	383	10	US-09-756-283A-27	Sequence 27, Appl
19	838.5	39.7	409	11	US-09-214-592-27	Sequence 27, Appl
20	835	39.5	410	11	US-09-214-592-22	Sequence 22, Appl
21	834	39.5	412	11	US-09-214-592-24	Sequence 24, Appl
22	832	39.4	412	11	US-09-214-592-19	Sequence 19, Appl
23	832	39.4	412	14	US-10-028-158-21	Sequence 21, Appl
24	831.5	39.3	414	11	US-09-214-592-21	Sequence 21, Appl
25	828	39.2	412	10	US-09-756-283A-25	Sequence 25, Appl
26	816.5	38.6	414	10	US-09-756-283A-24	Sequence 24, Appl
27	816.5	38.6	414	11	US-09-214-592-18	Sequence 18, Appl
28	815.5	38.6	412	11	US-09-214-592-30	Sequence 30, Appl
29	804.5	38.1	304	10	US-09-756-283A-26	Sequence 26, Appl
30	758	35.9	139	14	US-10-002-278-8	Sequence 8, Appli
31	642	30.4	115	10	US-09-859-211-47	Sequence 47, Appl
32	642	30.4	115	10	US-09-880-708-25	Sequence 25, Appl
33	642	30.4	115	11	US-09-872-856-47	Sequence 47, Appl
34	642	30.4	115	15	US-10-335-483-29	Sequence 29, Appl
35	640	30.3	114	10	US-09-813-459-22	Sequence 22, Appl

```
36
      640
            30.3 114 14 US-10-115-406-21
                                                     Sequence 21, Appl
37
      640 30.3
                  114 15 US-10-154-333-23
                                                     Sequence 23, Appl
      638
           30.2
                   112 10 US-09-813-271B-2
                                                     Sequence 2, Appli
38
      638
           30.2 113 10 US-09-813-398-13
                                                     Sequence 13, Appl
39
40
      562
            26.6
                   98 12 US-10-187-394-1
                                                     Sequence 1, Appli
           25.7
                   116 14 US-10-115-406-24
      544
                                                     Sequence 24, Appl
41
           25.7
                   116 15 US-10-154-333-26
      544
                                                     Sequence 26, Appl
42
                   112 10 US-09-813-271B-8
43
      535
           25.3
                                                     Sequence 8, Appli
           23.9
44
      505
                   114
                       14 US-10-115-406-25
                                                     Sequence 25, Appl
45
      505 23.9
                   114 15 US-10-154-333-27
                                                     Sequence 27, Appl
```

ALIGNMENTS

```
RESULT 1
US-09-214-592-26
; Sequence 26, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
 APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
 CURRENT APPLICATION NUMBER: US/09/214,592A
 CURRENT FILING DATE: 1999-01-18
 NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
 SEQ ID NO 26
   LENGTH: 390
   TYPE: PRT
   ORGANISM: porcine
US-09-214-592-26
 Query Match
                     96.3%; Score 2035; DB 11; Length 390;
 Best Local Similarity 97.0%; Pred. No. 1.9e-182;
 Matches 386; Conservative
                          1; Mismatches
                                          3;
                                             Indels
                                                      8; Gaps
                                                                 1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMLESGNQI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
```

```
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           111111111111111
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 2
US-09-214-592-29
; Sequence 29, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
 SEQ ID NO 29
   LENGTH: 390
   TYPE: PRT
   ORGANISM: ovine
US-09-214-592-29
 Query Match
                     91.5%; Score 1934; DB 11; Length 390;
 Best Local Similarity 91.7%; Pred. No. 5.9e-173;
 Matches 365; Conservative 10; Mismatches
                                        15;
                                            Indels
                                                       Gaps
                                                              1;
Qу
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
           Db
         1 MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
           Db
         61 SPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
           121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREEIEGFRLSAHCSCDSKDNTLQVDINGFS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qy
```

```
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Qу
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 3
US-10-087-268-2
; Sequence 2, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
  FILE REFERENCE: Fibrosis
 CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.1
; SEO ID NO 2
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Human
US-10-087-268-2
 Query Match
                     91.3%; Score 1931; DB 15; Length 390;
 Best Local Similarity
                   92.0%; Pred. No. 1.1e-172;
 Matches 366; Conservative 10; Mismatches
                                        14; Indels
                                                    8; Gaps
                                                              1;
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qy
           Db
         1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEOHVELYOKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           11111111111111111111111111111
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
```

```
293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
Qу
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 4
US-10-087-268-5
; Sequence 5, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
  APPLICANT: Jonsonn, Julie Ruth
  APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Human
US-10-087-268-5
 Query Match
                     91.0%; Score 1924; DB 15; Length 390;
 Best Local Similarity 91.7%; Pred. No. 5.1e-172;
 Matches 365; Conservative 10; Mismatches
                                       15; Indels
                                                       Gaps
Qу
         1 MAPSGLRLLPLLLVLLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
           Db
         1 MPPSGLRLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
        61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           1111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
```

```
RESULT 5
US-10-276-947-1
; Sequence 1, Application US/10276947
; Publication No. US20030176315A1
; GENERAL INFORMATION:
  APPLICANT: GLAXO GROUP LIMITED
  TITLE OF INVENTION: MEDICAL PRODUCTS
  FILE REFERENCE: PG3949
  CURRENT APPLICATION NUMBER: US/10/276,947
  CURRENT FILING DATE: 2002-11-21
  PRIOR APPLICATION NUMBER: GB 0012991.6
  PRIOR FILING DATE: 2000-05-26
  PRIOR APPLICATION NUMBER: GB 0100286.4
  PRIOR FILING DATE: 2001-01-05
  NUMBER OF SEQ ID NOS: 1
  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-276-947-1
 Query Match
                                      DB 12; Length 390;
                     90.9%; Score 1921;
 Best Local Similarity 91.7%; Pred. No. 9.8e-172;
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
                                                     8; Gaps
                                                               1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           111111111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
QУ
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
```

```
RESULT 6
US-09-214-592-33
; Sequence 33, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 33
   LENGTH: 390
   TYPE: PRT
   ORGANISM: simian
US-09-214-592-33
 Query Match
                     90.8%; Score 1919; DB 11; Length 390;
 Best Local Similarity
                     91.5%; Pred. No. 1.5e-171;
 Matches 364; Conservative 10; Mismatches
                                         16; Indels
                                                      8; Gaps
                                                                1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           11111111111:1
                                      Db
        181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
           1111111111111
Dh
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
QУ
           Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
```

```
US-09-214-592-17
; Sequence 17, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
 SOFTWARE:
; SEQ ID NO 17
   LENGTH: 391
   TYPE: PRT
   ORGANISM: human
US-09-214-592-17
 Query Match
                     90.5%; Score 1913.5; DB 11; Length 391;
 Best Local Similarity
                    91.5%; Pred. No. 5e-171;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                    9; Gaps
                                                              2;
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           1 MPPSGLRLLPLLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
        61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
           121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEOHVELYOKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
           181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
            241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEK 292
Db
        300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
Qу
           293 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGAS 352
Db
        360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           Db
        353 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
```

```
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-756-283A-23
                     90.4%; Score 1910; DB 10; Length 390;
 Query Match
 Best Local Similarity
                     91.2%; Pred. No. 1.1e-170;
 Matches 363; Conservative 10; Mismatches 17; Indels
                                                     8; Gaps
                                                               1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
           1 MPPSGLRLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHHEI 120
Dh
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            }}}}
Dh
        121 YDKFKOSTHSTYMFFNISELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           111111111111
Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLQSSRHRR-----ALDTNYCFSSTEKN 292
Qу
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Dh
Qу
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
US-09-214-592-28
; Sequence 28, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
```

```
APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 28
   LENGTH: 390
   TYPE: PRT
   ORGANISM: canine
US-09-214-592-28
 Query Match
                     89.8%; Score 1898; DB 11; Length 390;
 Best Local Similarity 90.7%; Pred. No. 1.4e-169;
 Matches 361; Conservative 12; Mismatches
                                        17; Indels
                                                     8; Gaps
                                                               1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
           Db
         1 MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLS 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEOHVELYOKYSNDSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINGFS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 SSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRORR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 10
US-09-214-592-20
; Sequence 20, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
; APPLICANT: Sato, CYasufumi
```

```
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
 SEQ ID NO 20
   LENGTH: 390
   TYPE: PRT
   ORGANISM: murine
US-09-214-592-20
 Query Match
                      87.0%; Score 1840; DB 11; Length 390;
 Best Local Similarity
                      86.9%; Pred. No. 3.9e-164;
 Matches 346; Conservative 15; Mismatches
                                          29;
                                             Indels
                                                         Gaps
                                                      8:
                                                                 1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            Db
          1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            |\cdot|
                  121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLORLKSSVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
             111111111111
Db
        241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 352
Qу
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Db
        353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 11
US-09-214-592-23
; Sequence 23, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
```

```
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 23
   LENGTH: 390
   TYPE: PRT
   ORGANISM: rat
US-09-214-592-23
 Query Match
                     87.0%; Score 1840; DB 11; Length 390;
                     86.9%; Pred. No. 3.9e-164;
 Best Local Similarity
 Matches 346; Conservative 14; Mismatches
                                         30; Indels
                                                      8; Gaps
                                                                1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
QУ
            1 MPPSGLRLLPLLLPLPULLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Dh
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
QУ
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Db
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
                  Db
        121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
             241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
           353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 12
US-09-214-592-25
; Sequence 25, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
 FILE REFERENCE: 11060
```

```
CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 25
   LENGTH: 315
   TYPE: PRT
   ORGANISM: bovine
US-09-214-592-25
 Query Match
                      74.6%; Score 1577; DB 11; Length 315;
 Best Local Similarity 91.3%; Pred. No. 1.4e-139;
 Matches 295; Conservative
                           9; Mismatches
                                          11; Indels
                                                      8: Gaps
                                                                 1:
         76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
Qу
            Db
          1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
        136 NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
Qу
            Db
         61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
        196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
Qу
            Db
        121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
        256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
Qу
            181 PFLLLMATPLERAQHLHSSRHRR------ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 232
Db
        316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
Qу
            233 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 292
Dh
        376 YYVGRKPKVEOLSNMIVRSCKCS 398
Qу
            Db
        293 YYVGRKPKVEOLSNMIVRSCKCS 315
RESULT 13
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
 APPLICANT: Chernajovsky, Yuti
 APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
   LENGTH: 455
   TYPE: PRT
   ORGANISM: Artificial Sequence
```

```
FEATURE:
   OTHER INFORMATION: LAP-mIFN
                            construct
US-09-756-283A-20
                      59.7%; Score 1262.5; DB 10; Length 455;
 Query Match
 Best Local Similarity
                     90.5%; Pred. No. 8.2e-110;
 Matches 248; Conservative 10; Mismatches
                                         15; Indels
                                                      1; Gaps
                                                                 1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEOHVELYOKYSNDSW 179
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
            Db
        181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Qу
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHS 273
             Dh
        241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQS 274
RESULT 14
US-09-756-283A-22
; Sequence 22, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
 SEQ ID NO 22
   LENGTH: 447
   TYPE: PRT
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: mIFN -LAP construct
US-09-756-283A-22
 Query Match
                     53.9%; Score 1139; DB 10; Length 447;
 Best Local Similarity
                     87.0%; Pred. No. 3.1e-98;
 Matches 228; Conservative 10; Mismatches
                                          18; Indels
                                                      6;
                                                          Gaps
                                                                 3;
         14 PL-LWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGP 72
QУ
           | | | | | |
```

```
Db
        190 PLGLW----AGGGSAAALSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSQGEVPPGP 245
         73 LPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLY 132
Qу
            246 LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKOSTHSIY 305
Db
        133 MLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSD 191
Qу
            306 MFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEOHVELYOKYSNNSWRYLSNRLLAPSD 365
Db
        192 SPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIH 251
Qу
                             366 SPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGRRGDLATIH 425
Db
        252 GMNRPFLLLMATPLERAOHLHS 273
Qу
            426 GMNRPFLLLMATPLERAQHLQS 447
Db
RESULT 15
US-09-214-592-32
; Sequence 32, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
 NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 32
   LENGTH: 373
   TYPE: PRT
   ORGANISM: chicken
US-09-214-592-32
                      50.1%; Score 1059.5; DB 11; Length 373;
 Query Match
 Best Local Similarity 54.5%; Pred. No. 7e-91;
 Matches 208; Conservative 52; Mismatches
                                        99; Indels
                                                      23; Gaps
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
Qу
            2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
Db
         90 GES-VEPEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
             :: | |:
                      11::::11
         62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
Dh
        149 LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
            : :
Db
        121 LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
```

Qу 204 VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258 Db 181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239 259 LLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFRKDLGW 316 QУ Db 240 LAMALPAERANELHSARRRRD------LDTDYCFGPGTDEKNCCVRPLYIDFRKDLOW 291 317 KWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVY 376 QУ 292 KWIHEPKGYMANFCMGPCPYIWSADTOYTKVLALYNOHNPGASAAPCCVPOTLDPLPIIY 351 Db 377 YVGRKPKVEQLSNMIVRSCKCS 398 QУ

Search completed: October 28, 2003, 09:27:59 Job time: 25.1473 secs

352 YVGRNVRVEQLSNMVVRACKCS 373

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:37:16; Search time 13.1517 Seconds

(without alignments)

2910.285 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Db

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result. Query Score Match Length DB ID No. Description 390 2 A27512 2038 96.4 1 transforming growt 2 2006.5 94.9 391 2 501413 transforming growt 1934 91.5 390 2 146463 3 transforming growt 1921 90.9 390 1 WFHU2 transforming growt 4 5 1919 90.8 390 2 A26960 transforming growt 89.8 390 2 JC4023 6 1898 transforming growt 7 87.0 390 1 WFMS2 1840 transforming growt 8 1840 87.0 390 2 S10219 transforming growt 9 1577 74.6 315 2 A40057 transforming growt 10 1059.5 50.1 373 2 A41918 transforming growt 11 876 41.4 412 2 A34939 transforming growt 12 873 41.3 382 2 B61036 transforming growt 409 2 S01825 13 838.5 39.7 transforming growt 410 2 A41397 835 39.5 14 transforming growt 410 2 A55706 39.5 15 834 transforming growt 16 832 39.4 412 2 A36169 transforming growt 17 831.5 39.3 414 1 WFMSB2 transforming growt 18 816.5 38.6 414 1 WFMKB2 transforming growt 19 816.5 38.6 414 2 A31249 transforming growt 20 816 38.6 413 1 WFXLB2 transforming growt 412 2 A39489 21 815.5 38.6 transforming growt 442 2 B31249 22 800.5 37.9 transforming growt 696 32.9 23 130 2 148196 transforming growt 24 482 22.8 112 2 A61439 transforming growt 25 281.5 13.3 425 2 147072 inhibin beta-A cha 26 278 13.2 424 1 WFPGBA inhibin beta-A cha 424 1 S31440 27 277 13.1 inhibin beta-A cha 425 1 S50898 276.5 13.1 28 inhibin beta-A cha 426 1 B24248 29 275 13.0 inhibin beta-A cha 424 1 B40905 30 273 12.9 inhibin beta-A cha 31 265 12.5 398 2 JH0688 bone morphogenetic 32 263.5 12.5 398 2 JH0687 bone morphogenetic 33 260.5 12.3 394 2 S45355 bone morphogenetic 34 259.5 12.3 396 1 BMHU2 bone morphogenetic 12.3 413 2 JC4862 35 259 activin beta-A cha 257 12.2 513 1 BMHU6 36 bone morphogenetic 37 255.5 12.1 510 2 A54798 Vg-1-related prote 11.9 393 2 S37073 38 252 bone morphogenetic 239.5 39 11.3 350 2 JC5241 activin beta E cha 40 239.5 11.3 420 2 149541 bone morphogenetic 237.5 41 11.2 455 2 A43918 TGF-beta-related p 232.5 408 2 JH0801 42 11.0 bone morphogenetic 2 A45056 43 232 11.0 402 osteogenic protein 408 2 538343 44 231.5 11.0 bone morphogenetic 367 2 JC4151 45 230.5 10.9 activin beta D cha

```
transforming growth factor beta-1 precursor - pig
N; Alternate names: TGF-beta
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Jun-1988 #sequence revision 05-Jun-1988 #text change 16-Jul-1999
C; Accession: A27512; A26356; I46657
R; Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A; Title: Sequence of the porcine transforming growth factor-beta precursor.
A; Reference number: A27512; MUID: 87174844; PMID: 3470708
A; Accession: A27512
A; Molecule type: mRNA
A; Residues: 1-390 < DER>
R; Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.;
Lucas, R.; Massaque, J.
Cell 48, 409-415, 1987
A; Title: The transforming growth factor-beta system, a complex pattern of cross-
reactive ligands and receptors.
A; Reference number: A90890; MUID: 87102890; PMID: 2879635
A; Accession: A26356
A; Molecule type: protein
A; Residues: 279-322 < CHE>
R; Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn,
M.B.; Roberts, A.B.
J. Biol. Chem. 263, 18313-18317, 1988
A; Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation.
A; Reference number: I46657; MUID: 89054010; PMID: 2461367
A; Accession: I46657
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-390 < KON>
A; Cross-references: GB: M23703; NID: q755044; PIDN: AAA64616.1; PID: q755045
C; Genetics:
A;Gene: TGFB; TGF-beta-1
C; Superfamily: inhibin
C; Keywords: growth factor
 Query Match
                        96.4%; Score 2038; DB 2; Length 390;
 Best Local Similarity
                        97.2%; Pred. No. 8.5e-156;
 Matches 387; Conservative 0; Mismatches
                                              3; Indels
                                                           8; Gaps
                                                                       1;
Qу
           1 MAPSGLRLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
             Db
           1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
             Db
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
             Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
         181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
             Db
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
```

A27512

```
241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           Db
        293 CCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 2
S01413
transforming growth factor beta-1 precursor - chicken
C; Species: Gallus gallus (chicken)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 24-Nov-1999
C; Accession: S01413
R; Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A; Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-
A; Reference number: S01413; MUID: 88335639; PMID: 3166520
A; Accession: S01413
A; Molecule type: DNA
A; Residues: 1-391 < JAK>
A; Cross-references: EMBL: X12373; NID: q63808; PIDN: CAA30933.1; PID: g63809
C; Superfamily: inhibin
C; Keywords: growth factor
                     94.9%; Score 2006.5; DB 2; Length 391;
 Query Match
                     96.2%; Pred. No. 2.9e-153;
 Best Local Similarity
 Matches 384: Conservative 0: Mismatches 6: Indels
                                                     9; Gaps
                                                               2;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGPGLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWG 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEIN-GF 239
Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHCSCDSKDNTLHVEINAGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
            241 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----
                                                --ALDTNYCFSSTEK 292
Db
        300 NCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGAS 359
Qу
```

```
293 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 352
Db
       360 AAPCCVPOALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
           353 AAPCCVPOALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
Db
RESULT 3
I46463
transforming growth factor beta-1 - sheep
C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 19-Dec-1997 #sequence revision 19-Dec-1997 #text_change 24-Nov-1999
C; Accession: I46463; S45115
R; Woodall, C.J.; McLaren, L.J.; Watt, N.J.
Gene 150, 371-373, 1994
A; Title: Sequence and chromosomal localisation of the gene encoding ovine latent
transforming growth factor-beta 1.
A; Reference number: I46463; MUID: 95121932; PMID: 7821809
A; Accession: I46463
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-390 < WOO>
A; Cross-references: EMBL: X76916; NID: g496648; PIDN: CAA54242.1; PID: g496649
A; Note: submitted to the EMBL Data Library, December 1993
C; Superfamily: inhibin
                     91.5%; Score 1934; DB 2; Length 390;
 Query Match
 Best Local Similarity 91.7%; Pred. No. 1.9e-147;
 Matches 365; Conservative 10; Mismatches
                                        15: Indels
                                                    8; Gaps
                                                              1;
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           1 MPPSGLRLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           61 SPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREEIEGFRLSAHCSCDSKDNTLQVDINGFS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
           241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
           293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
QУ
```

```
RESULT 4
WFHU2
transforming growth factor beta-1 precursor [validated] - human
N; Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C: Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text change 08-Dec-2000
C; Accession: A27513; A01395; A22290; I59664; S53444
R; Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A; Title: Intron-exon structure of the human transforming growth factor-beta
precursor gene.
A; Reference number: A27513; MUID: 87174845; PMID: 3470709
A; Accession: A27513
A; Molecule type: DNA
A; Residues: 1-390 < DER>
A; Cross-references: GB:X05839; GB:Y00112; NID:q37097; PIDN:CAA29283.1;
PID:q1212989
R; Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian,
R.K.; Roberts, A.B.; Sporn, M.B.; Goeddel, D.V.
Nature 316, 701-705, 1985
A; Title: Human transforming growth factor-beta complementary DNA sequence and
expression in normal and transformed cells.
A; Reference number: A01395; MUID: 85296301; PMID: 3861940
A; Accession: A01395
A; Molecule type: mRNA
A; Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 < DE2>
A; Cross-references: GB: X02812; GB: J05114; NID: g37092; PIDN: CAA26580.1;
PID:g37093
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic
core of an amino-terminal signal peptide
R; Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A; Title: Cellular receptors for type beta transforming growth factor. Ligand
binding and affinity labeling in human and rodent cell lines.
A; Reference number: A22290; MUID: 85131019; PMID: 2982829
A; Accession: A22290
A; Molecule type: protein
A; Residues: 279-295, 'XX', 298-301 < MAS>
R; Urushizaki, Y.; Niitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.;
Urushizaki, I.; Takahashi, Y.; Ito, H.
Tumor Res. 22, 41-55, 1987
A; Title: Cloning and expression of the gene for human transforming growth
factor-beta in Escherichia coli.
A; Reference number: 159664
A; Accession: I59664
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 279-390 < RES>
A; Cross-references: GB: M38449; NID: g339557; PIDN: AAA36735.1; PID: g339558
R;Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.;
Marshak, D.R.; Haley, J.D.
Biochem. J. 305, 87-92, 1995
A; Title: Physical and biological characterization of a growth-inhibitory
```

activity purified from the neuroepithelioma cell line A673.

```
A; Reference number: S53444; MUID: 95126934; PMID: 7826358
A; Accession: S53444
A; Status: preliminary
A; Molecule type: protein
A; Residues: 279-297 < STA>
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of identical polypeptide chains
linked by an interchain disulfide bond.
C; Genetics:
A; Gene: GDB: TGFB1; TGFB
A; Cross-references: GDB:120729; OMIM:190180
A; Map position: 19q13.2-19q13.2
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match
                      90.9%; Score 1921; DB 1; Length 390;
 Best Local Similarity
                     91.7%; Pred. No. 2.1e-146;
 Matches 365; Conservative 10; Mismatches
                                         15;
                                             Indels
                                                      8; Gaps
                                                                 1:
QУ
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Dh
          1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Dh
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR------ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
ÛУ
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
```

RESULT 5 A26960

transforming growth factor beta-1 precursor - green monkey C; Species: Cercopithecus aethiops (green monkey, grivet)

```
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 24-Nov-1999
C; Accession: A26960
R; Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987
A; Title: Cloning and sequence analysis of simian transforming growth factor-beta
CDNA.
A; Reference number: A26960; MUID: 87246074; PMID: 3474130
A; Accession: A26960
A; Molecule type: mRNA
A; Residues: 1-390 < SHA>
A; Cross-references: GB: M16658; NID: g176552; PIDN: AAA35369.1; PID: g176553
C; Superfamily: inhibin
C; Keywords: growth factor
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-390/Product: transforming growth factor beta #status predicted <MAT>
                      90.8%; Score 1919; DB 2; Length 390;
 Query Match
 Best Local Similarity
                     91.5%; Pred. No. 3e-146;
 Matches 364; Conservative 10; Mismatches
                                         16; Indels
                                                       8; Gaps
                                                                 1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGOILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSNSPEWLSFDVTGVVROWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
QУ
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 6
JC4023
transforming growth factor beta-1 - dog
C; Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1995 #sequence revision 14-Jul-1995 #text change 24-Nov-1999
C; Accession: JC4023
R; Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
```

Gene 155, 307-308, 1995

```
A; Title: Cloning of a canine cDNA homologous to the human transforming growth
factor-beta 1-encoding gene.
A; Reference number: JC4023; MUID: 95237630; PMID: 7721110
A; Accession: JC4023
A; Molecule type: mRNA
A; Residues: 1-390 <MAN>
A; Cross-references: GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
C; Comment: This factor plays a multifunctional role as a regulator of mammalian
cell growth and as a modulator of immune responses.
C:Genetics:
A;Gene: tqf-betal
C; Superfamily: inhibin
C; Keywords: growth factor; transforming protein
F;288-390/Product: transforming growth factor beta 1 #status predicted <MAT>
                      89.8%; Score 1898; DB 2; Length 390;
 Best Local Similarity
                     90.7%; Pred. No. 1.5e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels
                                                       8; Gaps
                                                                 1;
Qу
          1 MAPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            1 MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLS 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEOHVELYOKYSNDSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDTPEWLSFDVTGVVROWLSHGGEVEGFRLSAHCSCDSKDNTLOVDINGFS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            Db
        241 SSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRORR-----ALDTNYCFSSTEKN 292
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Dh
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 7
transforming growth factor beta-1 precursor - mouse
N; Alternate names: TGF type 2; TGF-beta
C; Species: Mus musculus (house mouse)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 24-Nov-1999
C; Accession: A01396
R; Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
```

```
A; Title: The murine transforming growth factor-beta precursor.
A; Reference number: A01396; MUID: 86168129; PMID: 3007454
A; Accession: A01396
A; Molecule type: mRNA
A; Residues: 1-390 < DER>
A; Cross-references: GB:M13177; NID:g201952; PIDN:AAA40423.1; PID:g201953
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic
core of an amino-terminal signal peptide
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of identical polypeptide chains
linked by an interchain disulfide bond.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen;
transformation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 87.0%; Score 1840; DB 1; Length 390; Best Local Similarity 86.9%; Pred. No. 6.6e-140;
 Matches 346; Conservative 15; Mismatches
                                           29:
                                               Indels
                                                        8; Gaps
                                                                   1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
QУ
            1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVROWLNOGDGIOGFRFSAHCSCDSKDNKLHVEINGIS 240
Dh
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Ov
              241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
Qу
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 360
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Dh
        353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
```

transforming growth factor beta-1 precursor - rat N;Alternate names: TGF type 2; TGF-beta

```
C; Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text change 24-Nov-1999
C; Accession: S10219; PT0023; S02267
R; Qian, S.W.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A; Title: cDNA cloning by PCR of rat transforming growth factor beta-1.
A; Reference number: S10219; MUID: 90272425; PMID: 2349108
A; Accession: S10219
A; Molecule type: mRNA
A; Residues: 1-390 < QIA>
A; Cross-references: EMBL: X52498; NID: g57341; PIDN: CAA36741.1; PID: g57342
R; Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
J. Biochem. 106, 304-310, 1989
A; Title: Purification and structural analysis of a latent form of transforming
growth factor-beta from rat platelets.
A; Reference number: PT0023; MUID: 90036779; PMID: 2478527
A; Accession: PT0023
A; Molecule type: protein
A; Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 < OKA>
R; Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989
A; Title: One of two subunits of masking protein in latent TGF-beta is a part of
pro-TGF-beta.
A; Reference number: S02267; MUID: 89121078; PMID: 2914605
A; Accession: S02267
A; Molecule type: protein
A; Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 < OK2 >
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; integrin binding
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-278/Domain: propeptide #status experimental <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       87.0%; Score 1840; DB 2; Length 390; 86.9%; Pred. No. 6.6e-140;
 Query Match
 Best Local Similarity
 Matches 346; Conservative 14; Mismatches
                                             30;
                                                  Indels
                                                         8; Gaps
                                                                       1;
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
             Db
           1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
             61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
                    Db
         121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
Qу
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
             Db
         181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
```

```
Db
          241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Qу
          301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
              Db
          293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASA 352
Qу
          361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
              Db
          353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
A40057
transforming growth factor beta-1 precursor - bovine (fragment)
N; Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or
dEGF; MGF-b; milk growth factor b; TGF-type II
C; Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1992 #sequence revision 28-Feb-1992 #text change 16-Jul-1999
C; Accession: A40057; A42320; A05284; A24322; B61439
R; Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker,
C.C.
Mol. Endocrinol. 1, 693-698, 1987
A; Title: Complementary deoxyribonucleic acid cloning of bovine transforming
growth factor-betal.
A; Reference number: A40057; MUID: 91042552; PMID: 3153459
A; Accession: A40057
A; Molecule type: mRNA
A; Residues: 1-315 < VAN>
A; Cross-references: GB: M36271; NID: q163747; PIDN: AAA30778.1; PID: q163748
R; Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A; Title: Purification and characterization of transforming growth factor-beta2.3
and -beta1.2 heterodimers from bovine bone.
A; Reference number: A42320; MUID: 92129307; PMID: 1733936
A; Accession: A42320
A; Molecule type: protein
A; Residues: 204-209, 'X', 211-217 < OGA>
R; Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan,
Y.C.E.; Stein, S.; Lehrman, S.R.; Smith, J.M.; Lamb, L.C.; Sporn, M.B.
Biochemistry 22, 5692-5698, 1983
A; Title: Purification and properties of a type beta transforming growth factor
from bovine kidney.
A; Reference number: A05284; MUID: 84104793; PMID: 6607069
A; Accession: A05284
A; Molecule type: protein
A; Residues: 204-218 < ROB>
R; Seyedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti,
A.; Siegel, N.R.; Galluppi, G.R.; Piez, K.A.
J. Biol. Chem. 261, 5693-5695, 1986
A; Title: Cartilage-inducing factor-A. Apparent identity to transforming growth
factor-beta.
A; Reference number: A24322; MUID: 86195954; PMID: 3754555
A; Accession: A24322
A; Molecule type: protein
A; Residues: 204-233 <SEY>
R; Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
```

```
A; Title: Separation, purification, and sequence identification of TGF-betal and
TGF-beta2 from bovine milk.
A; Reference number: A61439; MUID: 92189724; PMID: 1799413
A; Accession: B61439
A; Molecule type: protein
A; Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>
C; Comment: This polypeptide is composed of two polypeptide chains cross-linked
by disulfide bonds. It has been found in neoplastic and non-neoplastic tissues.
C; Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic
mitogenic activity, but in soft agar, it reacts synergistically with either type
I TFG or EGF, and induces cell proliferation. Cells grown in monolayer do not
respond in a similar manner to these growth factors, but morphologically do
acquire a transformed phenotype.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; heterodimer
F;204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match
                       74.6%; Score 1577; DB 2; Length 315;
 Best Local Similarity
                       91.3%; Pred. No. 6.3e-119;
 Matches 295; Conservative
                             9; Mismatches
                                           11;
                                                 Indels
                                                          8; Gaps
                                                                     1:
          76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLF 135
Qу
             1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
Db
Qу
         136 NTSELREAVPEPVLLSRAELRLKLKLKVEOHVELYOKYSNDSWRYLSNRLLAPSDSPEW 195
             61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
Db
         196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
Qу
            Db
         121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
         256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
Qу
             1111111
                                        Db
         181 PFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 232
         316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
QУ
             Db
         233 WKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALEPLPIV 292
         376 YYVGRKPKVEOLSNMIVRSCKCS 398
Qу
             Db
         293 YYVGRKPKVEOLSNMIVRSCKCS 315
RESULT 10
A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N; Alternate names: TGF-beta 4
C; Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C; Accession: A41918; A34941; S03110
R; Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992
```

```
A; Title: Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA.
A; Reference number: A41918; MUID: 92357039; PMID: 1353860
A; Accession: A41918
A; Molecule type: mRNA
A; Residues: 1-373 <BUR>
A;Cross-references: GB:M31160; GB:X08012; GB:S41706; NID:g1262437;
PIDN:AAB05637.1; PID:g1262438
A; Note: sequence extracted from NCBI backbone (NCBIN:110186, NCBIP:110187)
A; Note: this report corrects and reinterprets the sequence from reference A34941
R; Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 1186-1195, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic
acid encoding transforming growth factor beta-4 from chicken embryo
chondrocytes.
A; Reference number: A34941; MUID: 89112198; PMID: 2464131
A; Accession: A34941
A; Molecule type: mRNA
A; Residues: 'MDPMSIGPKSCGGSPWRPPGTAPWSIGSRRATASSSCSTSSRVRAEVGGRAL', 122-
209, 'D', 211-373 <JAK>
A; Cross-references: EMBL: X08012
A; Note: this sequence has been corrected in A41918
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor
F;1/Domain: signal sequence (fragment) #status predicted <SIG>
F;223-225/Region: cell attachment (R-G-D) motif
F;260-373/Product: transforming growth factor beta-4 #status predicted <MAT>
F;54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match
                       50.1%; Score 1059.5; DB 2; Length 373;
 Best Local Similarity 54.5%; Pred. No. 2.7e-77;
 Matches 208; Conservative 52; Mismatches
                                           99; Indels
                                                         23; Gaps
                                                                     8;
          30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
Qу
            2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
Db
          90 GES-VEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
                       62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWOPOSHSIFFVFNVSRARRG-GRPT 120
Db
         149 LLSRAELRLKLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
            Db
         121 LLHRAELRMLROKAAADSAGTEORLELYOGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
         204 VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
Qу
            :: 1 11
                                                 : [ ] [ ] : . ]
Db
         181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239
         259 LLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFRKDLGW 316
Qу
             Db
         240 LAMALPAERANELHSARRRD------LDTDYCFGPGTDEKNCCVRPLYIDFRKDLQW 291
         317 KWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVY 376
Qу
            Db
         292 KWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDPLPIIY 351
```

```
377 YVGRKPKVEQLSNMIVRSCKCS 398
Qу
              Db
          352 YVGRNVRVEQLSNMVVRACKCS 373
RESULT 11
A34939
transforming growth factor beta-3 precursor - chicken
C; Species: Gallus gallus (chicken)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C; Accession: A34939; S25850; S36125; S36124; I51181
R; Jakowlew, S.B.; Dillard, P.J.; Kondaiah, P.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 747-755, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a novel transforming
growth factor-beta messenger ribonucleic acid from chick embryo chondrocytes.
A; Reference number: A34939; MUID: 89096966; PMID: 3211158
A; Accession: A34939
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-412 < JAK>
A; Cross-references: GB: M31154; NID: q212758; PIDN: AAA49089.1; PID: q212759
R; Burt, D.W.; Paton, I.R.; Dey, B.R.
J. Mol. Endocrinol. 7, 175-183, 1991
A; Title: Comparative analysis of human and chicken transforming growth factor-
beta-2 and -beta-3 promoters.
A; Reference number: S25850; MUID: 92134496; PMID: 1840616
A; Accession: S25850
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 <BUR>
A; Cross-references: EMBL: X58127; NID: g63815; PIDN: CAA41128.1; PID: g63816
A; Accession: S36125
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 119-172 < BU2>
A; Cross-references: EMBL: X60055; NID: g396688; PIDN: CAA42653.1; PID: g396689
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
A; Accession: S36124
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 173-322, 'ELPT', 327-412 <BU3>
A; Cross-references: EMBL: X60091
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
1991
R; Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.;
Cubert, J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 6, 1285-1298, 1992
A; Title: Identification and characterization of the chicken transforming growth
factor-beta 3 promoter.
A; Reference number: I51181; MUID: 93024487; PMID: 1406706
A; Accession: I51181
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 <JA2>
A;Cross-references: GB:S46000; NID:g257172; PIDN:AAB23575.1; PID:g257173
```

C; Genetics:

```
A; Introns: 216/1; 252/1; 309/2; 360/3
A; Note: list of introns may be incomplete
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
F;74,142/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       41.4%; Score 876; DB 2; Length 412;
 Query Match
 Best Local Similarity 47.1%; Pred. No. 1.7e-62;
 Matches 198; Conservative 56; Mismatches 114; Indels 52; Gaps
                                                                    14;
          15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
                     1: | :|:
Db
          9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66
         75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNOIYDKF 124
Qу
              :||||||
                                       | ::
         67 YOILALYNSTRELL--EEMEEEKEESCSOENTESEYYAKEIHKFDMIOGLPEHNELGICP 124
Db
         125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
Qу
                                  | | | | | | | | | |
               ::: || |
                                                 : || :||:|
         125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180
Dh
         178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
Qу
               181 AKORYLSGRNVOTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240
Db
         230 N---TLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAQH--LHSSRHRR 278
Qу
                241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKOKDLHNPHLILMMLPPHRLESPTLGGORKKR 300
Db
         279 DYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIW 338
Qу
                   301 -----ALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYFANFCSGPCPYLR 352
Db
         339 SLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
             353 SADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
Db
RESULT 12
B61036
transforming growth factor beta-5 precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence revision 03-Feb-1994 #text change 16-Jul-1999
C; Accession: A34929; B61036
R; Kondaiah, P.; Sands, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn,
M.B.; Melton, D.A.
J. Biol. Chem. 265, 1089-1093, 1990
A; Title: Identification of a novel transforming growth factor-beta (TGF-beta5)
mRNA in Xenopus laevis.
A; Reference number: A34929; MUID: 90110090; PMID: 2295601
A; Accession: A34929
A; Molecule type: mRNA
```

A; Residues: 1-382 < KON>

```
A; Cross-references: GB: J05180; NID: g214821; PIDN: AAA49968.1; PID: g214822
R; Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert,
M.L.; Kondaiah, P.; Danielpour, D.; Kehrl, J.H.; Wahl, S.M.; Dawid, I.B.; Sporn,
M.B.
Growth Factors 2, 135-147, 1990
A; Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium
conditioned by Xenopus XTC cells.
A; Reference number: A61036; MUID: 90253806; PMID: 2340184
A; Accession: B61036
A; Molecule type: protein
A; Residues: 271-276, 'X', 278-284, 'XX', 287-299 < ROB>
C; Superfamily: inhibin
C; Keywords: growth factor
F;271-382/Product: transforming growth factor beta-5 #status experimental <MAT>
                       41.3%; Score 873; DB 2; Length 382;
 Best Local Similarity 46.9%; Pred. No. 2.6e-62;
 Matches 190; Conservative 55; Mismatches 122; Indels 38; Gaps
                                                                      11:
           9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
Qу
                            : : | | | | | | | |
           1 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS 59
Db
          69 PPGPLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNOIYDK 123
Qу
                :
                                                           |\cdot| :: |\cdot|
          60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
Db
         124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEOHVELYOKYSNDSW-- 179
Qу
                       ::|:||: || :
         116 ----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTTH 170
Db
         180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
Qу
                          : : | |
         171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
Db
         236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYC 293
Qy
             | | | | | | | | | | |
                                :|:|:: : | ||
                                              : ||| :|
         227 IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR-----GVGQEYC 277
Db
         294 FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ 353
Qу
             278 FGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQYSKVLSLYNQ 337
Db
         354 HNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
             Db
         338 NNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382
RESULT 13
S01825
transforming growth factor beta-3 precursor - pig
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1989 #sequence revision 30-Sep-1989 #text change 16-Jul-1999
C; Accession: S01825
R; Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee,
L.; Mason, A.J.; Miller, D.A.; Coffey, R.J.; Moses, H.L.; Chen, E.Y.
EMBO J. 7, 3737-3743, 1988
```

```
A; Title: A new type of transforming growth factor-beta, TGF-beta3.
A; Reference number: S01824; MUID: 89091120; PMID: 3208746
A; Accession: S01825
A; Molecule type: mRNA
A; Residues: 1-409 < DER >
A; Cross-references: EMBL: X14150; NID: q2127; PIDN: CAA32363.1; PID: q2128
C; Superfamily: inhibin
C; Keywords: growth factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-297/Domain: propeptide #status predicted <PRO>
F;298-409/Product: transforming growth factor beta-3 #status predicted <MAT>
 Query Match 39.7%; Score 838.5; DB 2; Length 409; Best Local Similarity 45.6%; Pred. No. 1.7e-59;
 Matches 190; Conservative 58; Mismatches 122; Indels 47; Gaps
                                                                   14;
Qу
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                     Db
          7 LVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGOILSKLRLTSPPDPSML--ANIP 64
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNOIYDKFKG 126
Qу
              Db
         65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124
QУ
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                125 ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
Dh
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             Db
         181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
Qу
         231 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAQH--LHSSRHRRDYK 281
              241 OEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAORKKR--- 297
Db
         282 DDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD 341
Qу
                Db
         298 ----ALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSAD 352
        342 TQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
QУ
            Db
         353 TTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTAKVEQLSNMVVKSCKCS 409
RESULT 14
A41397
transforming growth factor beta-3 precursor - mouse
C; Species: Mus musculus (house mouse)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text change 16-Jul-1999
C; Accession: A41397; A61039; A61225
R; Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A; Title: Complementary DNA cloning of the murine transforming growth factor-
beta3 (TGFbeta3) precursor and the comparative expression of TGFbeta3 and
TGFbetal messenger RNA in murine embryos and adult tissues.
```

A; Reference number: A41397; MUID: 90190650; PMID: 2628730

```
A; Accession: A41397
A; Molecule type: mRNA
A; Residues: 1-410 <MIL>
A; Cross-references: GB: M32745; NID: g201949; PIDN: AAA40422.1; PID: g201950
R; Denhez, F.; Lafyatis, R.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Growth Factors 3, 139-146, 1990
A; Title: Cloning by polymerase chain reaction of a new mouse TGF-beta, mTGF-
beta3.
A; Reference number: A61039; MUID: 91000714; PMID: 2206556
A; Accession: A61039
A; Molecule type: mRNA
A; Residues: 1-410 < DEN>
R; Watrin, F.; Scotto, L.; Assoian, R.K.; Wolgemuth, D.J.
Cell Growth Differ. 2, 77-83, 1991
A; Title: Cell lineage specificity of expression of the murine transforming
growth factor beta-3 and transforming growth factor beta-1 genes.
A; Reference number: A61225; MUID: 91299576; PMID: 2069871
A; Accession: A61225
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 285-410 <WAT>
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-298/Domain: propeptide #status predicted <PRO>
F;259-261/Region: cell attachment (R-G-D) motif
F;299-410/Product: transforming growth factor beta-3 #status predicted <MAT>
F;72,133,140/Binding site: carbohydrate (Asn) (covalent) #status predicted
  Query Match
                        39.5%; Score 835; DB 2; Length 410;
 Best Local Similarity 45.2%; Pred. No. 3.3e-59;
 Matches 188; Conservative 58; Mismatches 126; Indels
                                                            44; Gaps
                                                                       13:
Qу
          15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                        Db
           7 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGOILSKLRLTSPPEPSVMT--HVP 64
          75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNOIYDKFKG 126
Qу
                        1::
Db
          65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYOKYSND----S 178
Qу
                 :: || | : :
                                   | | | | | : | | :
                                                  : || :||:|
Db
         125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
                        ||: : |
Db
         181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 240
         231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAOHLHSSRHRRDYKD 282
Qу
                : :: | ::
                              : | |:|| |
Db
         241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK---- 296
         283 DDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342
Qу
                Db
         297 -- KRALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADT 354
```

```
Qу
         343 QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
              Db
         355 THSTVLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEOLSNMVVKSCKCS 410
RESULT 15
A55706
transforming growth factor beta-3 precursor - rat
C; Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text change 16-Jul-1999
C; Accession: A55706; B40699; S36042
R; Wang, J.; Kuliszewski, M.; Yee, W.; Sedlackova, L.; Xu, J.; Tseu, I.; Post, M.
J. Biol. Chem. 270, 2722-2728, 1995
A; Title: Cloning and expression of glucocorticoid-induced genes in fetal rat
lung fibroblasts. Transforming growth factor-beta-3.
A; Reference number: A55706; MUID: 95155340; PMID: 7852342
A; Accession: A55706
A; Molecule type: mRNA
A; Residues: 1-410 <WAN>
A; Cross-references: GB: U03491
A; Note: it is uncertain whether Met-1 is the initiator
R;McKinnon, R.D.; Piras, G.; Ida Jr., J.A.; Dubois-Dalcq, M.
J. Cell Biol. 121, 1397-1407, 1993
A; Title: A role for TGF-beta in oligodendrocyte differentiation.
A; Reference number: A40699; MUID: 93286190; PMID: 8509457
A; Accession: B40699
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 157-211 < MCK>
A; Cross-references: EMBL: X71903; NID: g311326; PIDN: CAA50722.1; PID: g311327
C; Superfamily: inhibin
 Query Match
                       39.5%; Score 834; DB 2; Length 410;
 Best Local Similarity
                       45.2%; Pred. No. 3.9e-59;
 Matches 188; Conservative 58; Mismatches 126; Indels 44; Gaps
                                                                     13:
Qу
          15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                     Db
           7 LVVLALLNLATVSLSLSTCTTLDFGHIKKKRVEAIRGOILSKLRLTSPPEPSVMT--HVP 64
          75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNOIYDKFKG 126
Qу
               |::
Db
          65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
Qу
                :: || | : :
                                 : || :||:|
Db
         125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
                      181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 240
Db
         231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRDYKD 282
Qу
                             : :: | ::
                                                             1:
Db
         241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGGQRK---- 296
```

283 DDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342

Qу

355 THSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 410

Search completed: October 28, 2003, 09:09:47

Job time : 15.1517 secs

Db

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:08:41; Search time 7.97725 Seconds

(without alignments)

2346.251 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEOLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41:*

9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2035	96.3	390	1	TGF1 PIG	P07200 sus scrofa
2	1934	91.5	390	1	TGF1 SHEEP	P50414 ovis aries
3	1921	90.9	390	1	TGF1_HUMAN	P01137 homo sapien
4	1919	90.8	390	1	TGF1 CERAE	P09533 cercopithec
5	1898	89.8	390	1	TGF1_CANFA	P54831 canis famil
6	1844	87.2	390	1	TGF1_HORSE	019011 equus cabal
7	1840	87.0	390	1	TGF1_MOUSE	P04202 mus musculu

```
8 1840 87.0 390 1 TGF1_RAT P17246 rattus norv 9 1831 86.6 390 1 TGF1_CAVPO O921y6 cavia porce 10 1577 74.6 315 1 TGF1_BOVIN P18341 bos taurus 11 1055.5 50.1 373 1 TGF1_CHICK P09531 gallus gallus gall 12 873 41.3 382 1 TGF1_XENLA P16176 xenopus lae 13 857 40.5 412 1 TGF3_CHICK P16047 gallus gall 14 838.5 39.7 409 1 TGF3_PIG P15203 sus scrofa 15 835 39.5 410 1 TGF3_MOUSE P17125 mus musculu 16 834 39.5 412 1 TGF3_RAT Q07258 rattus norv 17 832 39.4 412 1 TGF3_HUMAN P10600 homo sapien 18 831.5 39.3 414 1 TGF2_MOUSE P27090 mus musculu 19 816.5 38.6 414 1 TGF2_MOUSE P27090 mus musculu 20 816 38.6 413 1 TGF2_CHICK P3031 gallus gall 22 812.5 38.4 435 1 TGF2_FIG P09858 sus scrofa 23 812.5 38.4 442 1 TGF2_FIG P09858 sus scrofa 23 812.5 38.4 442 1 TGF2_PIG P09858 sus scrofa 24 482 22.8 112 1 TGF2_BOVIN P21214 bos taurus 25 339 16.0 375 1 GDF8_MELGA O42221 meleagris g 26 337 15.9 375 1 GDF8_CHICK O4220 gallus gall 29 324 15.3 376 1 GDF8_PIG O18831 sus scrofa 29 324 15.3 376 1 GDF8_PIG O18831 sus scrofa 29 324 15.3 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAT O35312 rattus norv 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 15.2 376 1 GDF8_RAP O18830 Ovis aries 31 322 14.8 374 1 GDF8_BAPP O18830 Ovis aries 31 322 14.8 374 1 GDF8_BAPP O18830 Ovis aries 32 276 5 13.1 424 1 HBA_RAPE P5029 292
```

ALIGNMENTS

```
RESULT 1
TGF1 PIG
    TGF1 PIG STANDARD;
                                 PRT; 390 AA.
AC
    P07200; P08832;
DT
    01-APR-1988 (Rel. 07, Created)
DT
     01-APR-1988 (Rel. 07, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
     Sus scrofa (Pig).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX
    NCBI TaxID=9823;
RN
    [1]
```

```
RΡ
     SEQUENCE FROM N.A.
RC
     TISSUE=Ovary;
     MEDLINE=87174844; PubMed=3470708;
RX
RA.
     Derynck R., Rhee L.;
RT
     "Sequence of the porcine transforming growth factor-beta precursor.";
RL
     Nucleic Acids Res. 15:3187-3187(1987).
RN
RΡ
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RC
     STRAIN=Miniature swine;
     MEDLINE=89054010; PubMed=2461367;
RX
     Kondaiah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
RA
RA
     Sporn M.B., Roberts A.B.;
     "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
RT
RT
     Evidence for alternate splicing and polyadenylation.";
     J. Biol. Chem. 263:18313-18317(1988).
RL
RN
     [3]
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RΡ
RX
     MEDLINE=88335639; PubMed=3166520;
RA
     Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
     "Nucleotide sequence of chicken transforming growth factor-beta 1
RT
RT
     (TGF-beta 1).";
     Nucleic Acids Res. 16:8730-8730(1988).
RL
RN
     SHOWS THAT REF.3 SEQUENCE IS FROM PIG.
RP
RA
     Jakowlew S.B.;
RL
     Unpublished observations (MAR-1996).
RN
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RP
RA
     Wimmers K., Chomdej S., Ponsuksili S., Schellander K.;
RT
     "Polymorphism in the porcine transforming growth factor beta 1
RT
     gene.";
RL
     Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN
     [6]
RP
     SEQUENCE OF 279-322.
     MEDLINE=87102890; PubMed=2879635;
RX
     Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RA
RA
     Lucas R., Massague J.;
     "The transforming growth factor-beta system, a complex pattern of
RT
     cross-reactive ligands and receptors.";
RT
     Cell 48:409-415(1987).
RL
     -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
CC
         PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
         TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
         HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
         ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
CC
         A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
     -!- SUBUNIT: Homodimer; disulfide-linked.
     -!- SUBCELLULAR LOCATION: Secreted.
CC
CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
     -!- CAUTION: REF.3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN
CC
CC
         WHITE LEGHORN, SEEMS (REF.4) TO ORIGINATE FROM PIG.
     ______
CC
CC
     This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
     between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

CC

CC

CC

```
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; Y00111; CAA68291.1; -.
DR
    EMBL; M23703; AAA64616.1; -.
    EMBL; X12373; CAA30933.1; -.
DR
    EMBL; AF461808; AAL57902.1; -.
DR
    PIR; A27512; A27512.
DR
    HSSP; P01137; 1KLA.
DR
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal; Polymorphism.
FT
    SIGNAL
                1
                      23
                             POTENTIAL.
FT
    PROPEP
                24
                      278
FT
               279
    CHAIN
                    390
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID 285
                    294
                             BY SIMILARITY.
    DISULFID 293
                    356
FT
                             BY SIMILARITY.
FT
                             BY SIMILARITY.
    DISULFID 322
                    387
    DISULFID 326 389 BY SIMILARITY.

DISULFID 355 355 INTERCHAIN (BY SIMILARITY).

CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
FT
FT
FT
FT
FT
    SITE
              244
                     246
                             CELL ATTACHMENT SITE (POTENTIAL).
    VARIANT
FT
              114
                     114
                              L -> V.
    CONFLICT
FT
               6
                      7
                              LR -> PG (IN REF. 3).
    CONFLICT
              180
FT
                     180
                              R \rightarrow G (IN REF. 3).
FT
    CONFLICT
               237
                     237
                             N \rightarrow NA (IN REF. 3).
SQ
    SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;
 Query Match
                       96.3%; Score 2035; DB 1; Length 390;
 Best Local Similarity 97.0%; Pred. No. 9e-154;
 Matches 386; Conservative 1; Mismatches 3; Indels 8; Gaps
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
             Db
           1 MPPSGLRLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
QУ
             Db
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMLESGNQI 120
Qу
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYOKYSNDSWR 180
             Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
```

```
Db
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
QУ
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
             Db
         241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRR-----ALDTNYCFSSTEKN 292
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
QУ
             Db
         293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Qу
         361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 2
TGF1 SHEEP
    TGF1 SHEEP
ΙD
                  STANDARD;
                                 PRT; 390 AA.
AC
    P50414;
DT
    01-OCT-1996 (Rel. 34, Created)
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
    Ovis aries (Sheep).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
    Bovidae; Caprinae; Ovis.
OX
    NCBI TaxID=9940;
RN
     [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=95121932; PubMed=7821809;
RA
    Woodall C.J., McLaren L.J., Watt N.J.;
RT
     "Sequence and chromosomal localisation of the gene encoding ovine
RT
    latent transforming growth factor-beta 1.";
RL
    Gene 150:371-373(1994).
RN
     [2]
RP
    SEQUENCE OF 281-390 FROM N.A.
RC
    STRAIN=Merino; TISSUE=Skin;
RX
    MEDLINE=95268698; PubMed=7749621;
RA
    Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
RT
     "Growth factor expression in skin during wool follicle development.";
RL
    Comp. Biochem. Physiol. 110B:697-705(1995).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
CC
CC
    use by non-profit institutions as long as its content is in no way
```

```
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
    CC
DR
    EMBL; X76916; CAA54242.1; -.
DR
    EMBL; L36038; AAA31526.1; -.
    PIR; I46463; I46463.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF_cysknot.
DR
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; \overline{1}.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
    SIGNAL
               1
                    23
                             POTENTIAL.
FT
    PROPEP
              24
                    278
                             POTENTIAL.
                             TRANSFORMING GROWTH FACTOR BETA 1.
FT
    CHAIN
              279
                    390
FT
    DISULFID
              285
                    294
                            BY SIMILARITY.
    DISULFID 293
                   356
FT
                            BY SIMILARITY.
FT
    DISULFID 322
                   387
                            BY SIMILARITY.
FT
    DISULFID
             326
                   389
                            BY SIMILARITY.
FT
    DISULFID
             355
                   355
                            INTERCHAIN (BY SIMILARITY).
FT
                    82
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
              82
FT
    CARBOHYD
              136
                    136
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
             176
                    176
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
              244
                    246
                           CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE 390 AA; 44291 MW; 1C247299484D0E57 CRC64;
                      91.5%; Score 1934; DB 1; Length 390;
 Query Match
 Best Local Similarity 91.7%; Pred. No. 9e-146;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                        8; Gaps
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGOILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYOKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREEIEGFRLSAHCSCDSKDNTLOVDINGFS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
```

```
Qу
          301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
              Db
          293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 352
QУ
          361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
              Db
          353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 3
TGF1 HUMAN
    TGF1 HUMAN
ID
                   STANDARD;
                                  PRT;
                                         390 AA.
AC
     P01137; Q9UCG4;
DT
     21-JUL-1986 (Rel. 01, Created)
     01-FEB-1991 (Rel. 17, Last sequence update)
DT
DT
     15-SEP-2003 (Rel. 42, Last annotation update)
DE
     Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
     TGFB1 OR TGFB.
OS
     Homo sapiens (Human).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
     NCBI TaxID=9606;
RN
     [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=87174845; PubMed=3470709;
RA
    Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
RT
     "Intron-exon structure of the human transforming growth factor-beta
RT
     precursor gene.";
RL
    Nucleic Acids Res. 15:3188-3189(1987).
RN
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=85296301; PubMed=3861940;
RA
    Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
RA
    Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RT
     "Human transforming growth factor-beta complementary DNA sequence and
RT
     expression in normal and transformed cells.";
RL
    Nature 316:701-705(1985).
RN
     [3]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Duodenum, and Eye:
RX
    MEDLINE=22388257; PubMed=12477932;
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA
     Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA
    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
RA
    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
RA
    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA
    Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
    Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA
    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA
    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA
    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA
RA
    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
```

```
RA
     Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT
     "Generation and initial analysis of more than 15,000 full-length
RT
     human and mouse cDNA sequences.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
     [4]
RP
     SEQUENCE OF 279-390 FROM N.A.
RC
     TISSUE=Carcinoma;
RA
     Urushizaki Y., Niitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
RA
     Urushizaki I., Takahashi Y., Ito H.;
RT
     "Cloning and expression of the gene for human transforming growth
RT
     factor-beta in Escherichia coli.";
RL
     Tumor Res. 22:41-55(1987).
RN
     [5]
     SEQUENCE OF 279-329.
RP
RC
     TISSUE=Bladder carcinoma;
RX
     MEDLINE=93229900; PubMed=8471846;
RA
     Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
RA
     Hu S., Westcott K.R.;
     "Recombinant human transforming growth factor-beta 1: expression by
RT
RT
     Chinese hamster ovary cells, isolation, and characterization.";
RL
     Protein Expr. Purif. 4:130-140(1993).
RN
RP
     SEQUENCE OF 279-301.
RX
     MEDLINE=85131019; PubMed=2982829;
RA
     Massague J., Like B.;
     "Cellular receptors for type beta transforming growth factor. Ligand
RT
     binding and affinity labeling in human and rodent cell lines.";
RT
RL
     J. Biol. Chem. 260:2636-2645(1985).
RN
     [7]
RP
     STRUCTURE BY NMR OF 279-390.
RX
     MEDLINE=93144319; PubMed=8424942;
RA
     Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA
     Torchia D.A.;
     "Transforming growth factor beta 1: NMR signal assignments of the
RT
RT
     recombinant protein expressed and isotopically enriched using Chinese
RT
     hamster ovary cells.";
RL
     Biochemistry 32:1152-1163(1993).
RN
     STRUCTURE BY NMR OF 279-390.
RP
RX
     MEDLINE=93144320; PubMed=8424943;
     Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA
RA
     Torchia D.A.;
RT
     "Transforming growth factor beta 1: secondary structure as determined
RT
     by heteronuclear magnetic resonance spectroscopy.";
RL
     Biochemistry 32:1164-1171(1993).
RN
     [9]
RP
     STRUCTURE BY NMR OF 279-390.
RX
     MEDLINE=96266150; PubMed=8679613;
RA
     Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA
     Torchia D.A.;
RT
     "Transforming growth factor beta 1: three-dimensional structure in
RT
     solution and comparison with the X-ray structure of transforming
RT
     growth factor beta 2.";
```

```
RL
    Biochemistry 35:8517-8534(1996).
CC
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC
        CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; X05839; CAA29283.1; -.
    EMBL; X05840; CAA29283.1; JOINED.
DR
    EMBL; X05843; CAA29283.1; JOINED.
DR
    EMBL; X05844; CAA29283.1; JOINED.
DR
DR
    EMBL; X05849; CAA29283.1; JOINED.
DR
    EMBL; X05850; CAA29283.1; JOINED.
DR
    EMBL; X02812; CAA26580.1; ALT SEQ.
DR
    EMBL; BC001180; AAH01180.1; -.
DR
    EMBL; BC000125; AAH00125.1; -.
    EMBL; BC022242; AAH22242.1; -.
DR
DR
    EMBL; M38449; AAA36735.1; -.
DR
    PIR; A27513; WFHU2.
DR
    PDB; 1KLA; 17-AUG-96.
DR
    PDB; 1KLC; 17-AUG-96.
DR
    PDB; 1KLD; 17-AUG-96.
DR
    Genew; HGNC:11766; TGFB1.
    MIM; 190180; -.
DR
    GO; GO:0006916; P:anti-apoptosis; TAS.
DR
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
                               POTENTIAL.
FT
    SIGNAL
                       23
                1
FT
    PROPEP
                24
                      278
FT
    CHAIN
                279
                      390
                                TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
               285
                      294
FT
    DISULFID 293
                      356
FT
    DISULFID
             322
                      387
FT
    DISULFID
               326
                      389
FT
    DISULFID
             355
                     355
                              INTERCHAIN.
```

```
FT
    CARBOHYD
               82
                    82
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              136
                    136
FΤ
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
              176
                    176
FT
                    246
                            CELL ATTACHMENT SITE (POTENTIAL).
    SITE
              244
FT
    CONFLICT
              10
                    10
                            L -> P (IN REF. 2).
FT
                            R \rightarrow RR (IN REF. 2).
    CONFLICT
              159
                    159
FT
    STRAND
                    281
              281
FT
    TURN
              282
                    287
FT
    STRAND
              294
                    296
FT
    STRAND
              300
                    300
FT
    TURN
              302
                    305
FT
    STRAND
              313
                    313
    STRAND
FT
              317
                    317
FT
    STRAND
              321
                    323
FT
    HELIX
              335
                    346
FT
    TURN
              348
                    349
FT
                    370
    STRAND
              358
                    372
FT
    TURN
              371
FT
    STRAND
              373
                    387
SQ
    SEQUENCE
             390 AA; 44341 MW; 75391614250288FE CRC64;
                      90.9%; Score 1921; DB 1;
 Query Match
 Best Local Similarity
                     91.7%; Pred. No. 9.6e-145;
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
                                                      8;
                                                         Gaps
                                                                1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLLLLLLLLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Ov
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QУ
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Dh
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 4
TGF1 CERAE
    TGF1 CERAE
                STANDARD;
                             PRT:
```

390 AA.

```
AC
    P09533;
DT
    01-MAR-1989 (Rel. 10, Created)
DT
    01-MAR-1989 (Rel. 10, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
    Cercopithecus aethiops (Green monkey) (Grivet).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC
OC
    Cercopithecinae; Cercopithecus.
OX
    NCBI TaxID=9534;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RX
    MEDLINE=87246074; PubMed=3474130;
RA
    Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
    "Cloning and sequence analysis of simian transforming growth
RT
RT
    factor-beta cDNA.";
RL
    DNA 6:239-244(1987).
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION,
CC
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC
        CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
    _____
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    ______
    EMBL; M16658; AAA35369.1; -.
DR
    PIR; A26960; A26960.
DR
DR
    HSSP; P01137; 1KLA.
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
    SIGNAL
               1
                      16
                              POTENTIAL.
                17
                      278
FT
    PROPEP
               279
                      390
                               TRANSFORMING GROWTH FACTOR BETA 1.
FT
    CHAIN
                              BY SIMILARITY.
    DISULFID 285 294
FT
    DISULFID 293 356
                              BY SIMILARITY.
FT
    DISULFID 322 387
                              BY SIMILARITY.
FT
```

```
FT
                    355
                            INTERCHAIN (BY SIMILARITY).
    DISULFID
              355
FT
    CARBOHYD
              82
                    82
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
    CARBOHYD
              136
                    136
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
              176
                    176
                            CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
              244
                    246
             390 AA; 44356 MW; DFF63E2BAB44320E CRC64;
SO
    SEQUENCE
 Query Match
                     90.8%; Score 1919; DB 1; Length 390;
                     91.5%; Pred. No. 1.4e-144;
 Best Local Similarity
 Matches 364; Conservative 10; Mismatches
                                                      8;
                                         16; Indels
                                                          Gaps
                                                                 1;
Qу
          1 MAPSGLRLLPLLUPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
QУ
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
QУ
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            353 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
Db
RESULT 5
TGF1 CANFA
ΙD
    TGF1 CANFA
                STANDARD;
                             PRT;
                                   390 AA.
    P54831;
AC
DT
    01-OCT-1996 (Rel. 34, Created)
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DE
GN
    TGFB1.
OS
    Canis familiaris (Dog).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
    NCBI TaxID=9615;
OX
RN
    SEQUENCE FROM N.A.
RP
RC
    TISSUE=Jugular vein endothelial;
```

BY SIMILARITY.

FT

DISULFID

326

389

```
MEDLINE=95237630; PubMed=7721110;
RX
RA
    Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;
RT
    "Cloning of a canine cDNA homologous to the human transforming growth
RT
    factor-beta 1-encoding gene.";
RL
    Gene 155:307-308(1995).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    _____
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
    _____
CC
DR
    EMBL; L34956; AAA51458.1; -.
DR
    PIR; JC4023; JC4023.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
                1
                      23
                              POTENTIAL.
    SIGNAL
                      278
                               BY SIMILARITY.
FT
    PROPEP
                24
                      390
                               TRANSFORMING GROWTH FACTOR BETA 1.
FT
    CHAIN
                279
FT
                     294
                              BY SIMILARITY.
    DISULFID
               285
                              BY SIMILARITY.
FT
               293
                     356
    DISULFID
                              BY SIMILARITY.
FT
               322
                      387
    DISULFID
                              BY SIMILARITY.
FT
               326
                     389
    DISULFID
FT
    DISULFID
              355
                     355
                               INTERCHAIN.
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               82
                      82
FT
    CARBOHYD
               136
                      136
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               176
                      176
                              CELL ATTACHMENT SITE (POTENTIAL).
FT
                      246
    SITE
                244
SQ
    SEQUENCE 390 AA; 44185 MW; EB4780E88B7B590E CRC64;
                        89.8%; Score 1898; DB 1; Length 390;
  Query Match
  Best Local Similarity 90.7%; Pred. No. 6.4e-143;
  Matches 361; Conservative 12; Mismatches 17; Indels
                                                                        1;
```

```
Db
          1 MPPSGLRLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLS 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQ1 120
Qу
            Db
         61 SPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
            121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEOHVELYOKYSNDSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDTPEWLSFDVTGVVROWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINGFS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 SSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQRR-----ALDTNYCFSSTEKN 292
Db
Qу
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
            293 CCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
        361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
            353 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 6
TGF1 HORSE
ΙD
    TGF1 HORSE
                STANDARD;
                             PRT:
                                   390 AA.
AC
    019011;
    15-JUL-1998 (Rel. 36, Created)
DΤ
    15-JUL-1998 (Rel. 36, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DΕ
GN
    TGFB1.
    Equus caballus (Horse).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC
OX
    NCBI TaxID=9796;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Lymph node;
    MEDLINE=98185507; PubMed=9524819;
RX
    Penha-Goncalves M.N., Onions D.E., Nicolson L.;
RA
    "Cloning and sequencing of equine transforming growth factor-beta 1
RT
RT
    (TGF beta-1) cDNA.";
    DNA Seq. 7:375-378(1997).
RL
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
       PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
CC
       TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
       HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
       ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
       A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
```

```
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
    ______
CC
DR
    EMBL; X99438; CAA67801.1; -.
DR
    HSSP; P01137; 1KLA.
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb_propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
              1
                    23
FT
    SIGNAL
                            POTENTIAL.
              24
FT
    PROPEP
                    278
                            BY SIMILARITY.
FT
    CHAIN
              279
                   390
                            TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID 285 294
                           BY SIMILARITY.
    DISULFID 293 356
DISULFID 322 387
DISULFID 326 389
                           BY SIMILARITY.
FT
                           BY SIMILARITY.
FT
                           BY SIMILARITY.
FT
FT
    DISULFID 355 355
                            INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
              82
                    82
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD 136 136
FT
    CARBOHYD
             176 176
    SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;
SQ
 Query Match
                      87.2%; Score 1844; DB 1; Length 390;
 Best Local Similarity 88.4%; Pred. No. 1.2e-138;
 Matches 352; Conservative 12; Mismatches 26; Indels
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
               Db
        121 YKTVETGSHSIYMFFNTSELRAAVPDPMLLSRAELRLLRLKLSVEOHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGFRLSAHCSCDSKDNTLRVGINGFS 240
```

```
Qу
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
             Db
         241 SSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRHRR-----ALDTNYCFSSTEKN 292
Ov
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
             293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
QУ
         361 APCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
             353 APCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 7
TGF1 MOUSE
ID
    TGF1 MOUSE
                STANDARD; PRT; 390 AA.
AC
    P04202;
DT
    20-MAR-1987 (Rel. 04, Created)
DT
    20-MAR-1987 (Rel. 04, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
    NCBI TaxID=10090;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RX
    MEDLINE=86168129; PubMed=3007454;
RA
    Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT
    "The murine transforming growth factor-beta precursor.";
RL
    J. Biol. Chem. 261:4377-4379(1986).
RN
    [2]
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=BALB/c;
    MEDLINE=96096545; PubMed=8522200;
RX
    Guron C., Sudarshan C., Raghow R.;
RA
RT
    "Molecular organization of the gene encoding murine transforming
RT
    growth factor beta 1.":
RL
    Gene 165:325-326(1995).
RN
    [3]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=C57BL/6, and NOD/LT; TISSUE=Spleen;
RA
    Poirot L., Benoist C., Mathis D.;
RT
    "Transforming growth factor-beta 1 sequence and expression: no
RT
    difference between NOD/Lt and C57Bl/6 mouse strains.";
RL
    Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
```

```
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
     EMBL; M13177; AAA40423.1; -.
DR
DR
    EMBL; L42462; AAB00138.1; -.
DR
    EMBL; L42456; AAB00138.1; JOINED.
DR
    EMBL; L42457; AAB00138.1; JOINED.
DR
    EMBL; L42458; AAB00138.1; JOINED.
DR
    EMBL; L42459; AAB00138.1; JOINED.
DR
    EMBL; L42460; AAB00138.1; JOINED.
    EMBL; L42461; AAB00138.1; JOINED.
DR
DR
     EMBL; AJ009862; CAA08900.1; -.
DR
    PIR; A01396; WFMS2.
DR
    HSSP; P01137; 1KLA.
DR
    MGD; MGI:98725; Tgfb1.
DR
    GO; GO:0005578; C:extracellular matrix; IDA.
    GO; GO:0006954; P:inflammatory response; IMP.
DR
    GO; GO:0007515; P:lymph gland development; IMP.
DR
DR
    GO; GO:0008220; P:necrosis; IMP.
DR
    GO; GO:0016202; P:regulation of myogenesis; IDA.
DR
    InterPro; IPR002400; GF cysknot.
DR
     InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
     InterPro; IPR001111; TGFb N.
DR
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     Pfam; PF00688; TGFb propeptide; 1.
DR
     PRINTS; PR00438; GFCYSKNOT.
DR
     PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
                        23
    SIGNAL
                 1
                                 POTENTIAL.
FT
    PROPEP
                 24
                       278
                                 TRANSFORMING GROWTH FACTOR BETA 1.
FT
                279
                       390
    CHAIN
FT
    DISULFID
              285
                       294
                                BY SIMILARITY.
FT
    DISULFID
              293
                       356
                                BY SIMILARITY.
                                BY SIMILARITY.
FT
    DISULFID
               322
                      387
               326
                                 BY SIMILARITY.
FT
    DISULFID
                       389
                355
                       355
                                 INTERCHAIN (BY SIMILARITY).
FT
    DISULFID
FT
    CARBOHYD
                82
                       82
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
                                 N-LINKED (GLCNAC. . .) (POTENTIAL) .
                136
FT
    CARBOHYD
                       136
FT
    CARBOHYD
                176
                       176
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
                244
                       246
                                CELL ATTACHMENT SITE (POTENTIAL).
    SEQUENCE
               390 AA; 44310 MW; 4381A51B711D689E CRC64;
SQ
  Ouery Match
                         87.0%; Score 1840; DB 1;
                                                     Length 390;
 Best Local Similarity
                         86.9%; Pred. No. 2.5e-138;
 Matches 346; Conservative 15; Mismatches 29; Indels
                                                                8; Gaps
                                                                            1:
            1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
```

```
Db
          1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
            Db
        121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            Db
        181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
              241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Db
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
QУ
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
QУ
            Db
        353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 8
TGF1 RAT
    TGF1 RAT
                 STANDARD;
                              PRT;
                                    390 AA.
ΙD
AC
    P17246;
DT
    01-AUG-1990 (Rel. 15, Created)
    01-AUG-1990 (Rel. 15, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DE
    TGFB1.
GN
OS
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
    NCBI TaxID=10116;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=Sprague-Dawley; TISSUE=Heart;
RX
    MEDLINE=90272425; PubMed=2349108;
RA
    Qian S.W., Kondaiah P., Roberts A.B., Sporn M.B.;
RT
    "cDNA cloning by PCR of rat transforming growth factor beta-1.";
RL
    Nucleic Acids Res. 18:3059-3059(1990).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
       HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
       ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
       A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; X52498; CAA36741.1; -.
DR
    PIR; S10219; S10219.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                      23
                              POTENTIAL.
    PROPEP
FT
               24
                     278
FT
    CHAIN
               279
                     390
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
              285
                     294
                             BY SIMILARITY.
FT
    DISULFID
              293
                     356
                             BY SIMILARITY.
FT
    DISULFID
              322
                     387
                              BY SIMILARITY.
FT
    DISULFID
               326
                     389
                              BY SIMILARITY.
FT
    DISULFID
              355
                     355
                              INTERCHAIN (BY SIMILARITY).
FT
               82
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
                     82
FT
    CARBOHYD
              136
                     136
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              176
                     176
                             CELL ATTACHMENT SITE (POTENTIAL).
FΤ
              244
    SITE
                     246
    SEQUENCE
            390 AA; 44329 MW; 5E21108ED50D853C CRC64;
SQ
 Query Match
                       87.0%; Score 1840; DB 1; Length 390;
 Best Local Similarity
                       86.9%; Pred. No. 2.5e-138;
 Matches 346; Conservative 14; Mismatches
                                            30; Indels
                                                         8; Gaps
                                                                    1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
                 Db
        121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
```

CC

```
Qу
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
               1111111111111111
Db
         241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKN 292
Qу
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASA 360
             Db
         293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
QУ
         361 APCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
             Db
         353 SPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
TGF1 CAVPO
ΙD
    TGF1 CAVPO
                   STANDARD;
                                 PRT;
                                        390 AA.
AC
    Q9Z1Y6; Q9QZB3; Q9R148;
DT
    16-OCT-2001 (Rel. 40, Created)
DT
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
    Cavia porcellus (Guinea pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
    NCBI TaxID=10141;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Hartley;
RA
    Jeevan A., McMurray D.N., Yoshimura T.;
RT
    "Guinea pig transforming growth factor-beta in peritoneal exudates
RT
    after BCG vaccination.";
    Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RI.
RN
    SEQUENCE OF 265-382 FROM N.A.
RP
    MEDLINE=99144670; PubMed=10025978;
RX
    Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RA
RT
    "Spontaneous cytokine gene expression in normal guinea pig blood and
RT
    tissues.";
    Cytokine 10:851-859(1998).
ŔĹ
RN
RΡ
    SEQUENCE OF 279-371 FROM N.A.
    STRAIN=Hartley; TISSUE=Trachea;
RC
RA
    Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
RA
    Sekizawa K.:
RT
    "Guinea-pig transforming growth factor-beta expression in injured
RT
    tracheal epithelium.";
RL
    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
        CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
    -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
```

```
CC
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    _____
DR
    EMBL; AF191297; AAF02780.1; -.
DR
    EMBL; AF097509; AAC83807.1; -.
DR
    EMBL; AF169347; AAD49347.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL 1 24
                             POTENTIAL.
FT
    PROPEP
               25
                     278
                              POTENTIAL.
FT
    CHAIN
             279 390
                             TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID 285 294
                             BY SIMILARITY.
                            BY SIMILARITY.
BY SIMILARITY.
                   356
    DISULFID 293
FT
FT
    DISULFID
             322
                    387
            326 389
                            BY SIMILARITY.
FT
    DISULFID
FT
    DISULFID 355 355
                             INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
              82
                     82
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
            136 136
    CARBOHYD 176
FT
                    176
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                   246
             244
                             CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
             279
FT
                   279
                             G \rightarrow P (IN REF. 3).
    CONFLICT
    CONFLICT 286 286
FT
                             F \rightarrow S (IN REF. 2).
    CONFLICT
FT
             309 309
                             K \rightarrow E (IN REF. 2).
FT
    CONFLICT
             322
                    322
                             C -> R (IN REF. 2).
FT
    CONFLICT
              350
                    350
                            A \rightarrow G (IN REF. 2).
SO
    SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0FF1 CRC64;
                      86.6%; Score 1831; DB 1; Length 390;
 Query Match
 Best Local Similarity 86.7%; Pred. No. 1.3e-137;
 Matches 345; Conservative 15; Mismatches 30; Indels
                                                         8; Gaps
                                                                     1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSRLRLLPLLLPLLWLLVLAPGRPASGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEPDYYAKEVTRVLMVDNSHNI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
```

```
Db
         121 YKSIETVAHSIYMFFNTSELREAVPDPLLLSRAELRMORLKLNVEQHVELYQKYSNNSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QУ
            181 YLSNQLLTPSDTPEWLSFDVTGVVRQWLSQGEELEGFRFSAHCSCDSKDNTLRVEINGIG 240
Db
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
              241 PKRRGDLAAIHGMNRPFLLLMATPLERAOHLHSSRHRR------GLDTNYCFSSTEKN 292
Db
Qу
         301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
             293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
Db
QУ
         361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Dh
         353 APCCVPQALEPLPIVYYVGRKAKVEQLSNMIVRSCKCS 390
RESULT 10
TGF1 BOVIN
ID
    TGF1 BOVIN
                  STANDARD;
                               PRT:
                                     315 AA.
    P18341;
AC
DT
    01-NOV-1990 (Rel. 16, Created)
    01-NOV-1990 (Rel. 16, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
GN
    TGFB1.
OS
    Bos taurus (Bovine).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
    Bovidae; Bovinae; Bos.
OC
OX
    NCBI TaxID=9913;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RX
    MEDLINE=91042552; PubMed=3153459;
    van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.,
RA
    Baker C.C.;
RA
    "Complementary deoxyribonucleic acid cloning of bovine transforming
RT
    growth factor-beta 1.":
    Mol. Endocrinol. 1:693-698(1987).
RT.
RN
    [2]
    SUBUNITS.
RP
    TISSUE=Bone;
RC
    MEDLINE=92129307; PubMed=1733936;
RX
    Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RA
RT
    "Purification and characterization of transforming growth factor-beta
    2.3 and -beta 1.2 heterodimers from bovine bone.";
RT
    J. Biol. Chem. 267:2325-2328(1992).
RL
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked. Heterodimers of TGF-beta 1/2
```

```
CC
        have been found in bone.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
CC
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
    -----
CC
DR
    EMBL; M36271; AAA30778.1; -.
DR
    PIR; A40057; A40057.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb_propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein.
FT
    NON TER
               1
FT
    PROPEP
                     203
               <1
FT
    CHAIN
               204
                     315
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
              210
                     219
                              BY SIMILARITY.
                            BY SIMILARITY.
FT
    DISULFID 218
                    281
FT
    DISULFID
            247
                     312
                             BY SIMILARITY.
FT
    DISULFID
            251
                     314
                             BY SIMILARITY.
FT
    DISULFID
               280
                     280
                             INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
               7
                     7
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
               61
                     61
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               101
                     101
                    171
FT
    SITE
              169
                             CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE 315 AA; 36269 MW; C2717A23D994E00E CRC64;
 Query Match
                       74.6%; Score 1577; DB 1; Length 315;
 Best Local Similarity 91.3%; Pred. No. 1.3e-117;
 Matches 295; Conservative 9; Mismatches 11; Indels
                                                       8; Gaps
Оy
         76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
            1:111111111111111 | 111111111111111111 | 1:1111 | 1:1111
Db
          1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
Qу
        136 NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
            Db
         61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
Qу
        196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
            Dh
        121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
```

```
Qу
         256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
             Db
         181 PFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 232
         316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
Qу
             Db
         233 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 292
QУ
         376 YYVGRKPKVEOLSNMIVRSCKCS 398
             1111111111111
Db
         293 YYVGRKPKVEQLSNMIVRSCKCS 315
RESULT 11
TGF1 CHICK
ID
    TGF1 CHICK STANDARD; PRT; 373 AA.
AC
    P09531;
DT
    01-MAR-1989 (Rel. 10, Created)
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
DE
    (Fragment).
    TGFB1.
GN
OS
    Gallus gallus (Chicken).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC
    Gallus.
OX
    NCBI TaxID=9031;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=White leghorn;
RX
    MEDLINE=89112198; PubMed=2464131;
RA
    Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT
    "Complementary deoxyribonucleic acid cloning of a messenger
RT
    ribonucleic acid encoding transforming growth factor beta 4 from
RT
    chicken embryo chondrocytes.";
    Mol. Endocrinol. 2:1186-1195(1988).
RL
RN
    [2]
RP
    REVISIONS.
RX
    MEDLINE=92357039; PubMed=1353860;
RA
    Burt D.W., Jakowlew S.B.:
RT
    "Correction: a new interpretation of a chicken transforming growth
    factor-beta 4 complementary DNA.";
RT
    Mol. Endocrinol. 6:989-992(1992).
RL
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
    CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
```

```
use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; M31160; AAB05637.1; -.
DR
    PIR; A41918; A41918.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb_propeptide; 1.
DR
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    NON TER
             1
FT
    SIGNAL
              <1
                     1
                            POTENTIAL.
FT
    PROPEP
              2
                    259
                           POTENTIAL.
                  373
277
FT
    CHAIN
              260
                            TRANSFORMING GROWTH FACTOR BETA 1.
    DISULFID 266
FT
                           BY SIMILARITY.
                           BY SIMILARITY.
FT
    DISULFID 276 339
FT
    DISULFID 305 370
                           BY SIMILARITY.
FT
    DISULFID 309 372
                           BY SIMILARITY.
    DISULFID 338
                   338
                           INTERCHAIN (BY SIMILARITY).
FT
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
             54
                    54
    CARBOHYD 109 109
FT
             153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
224 226 CELL ATTACHMENT SITE (POTENTIAL).
FT
    CARBOHYD
FT
    SITE
SQ
    SEQUENCE 373 AA; 42634 MW; 9903F3479C8552E5 CRC64;
                      50.1%; Score 1059.5; DB 1; Length 373;
 Query Match
 Best Local Similarity 54.5%; Pred. No. 1.5e-76;
 Matches 208; Conservative 52; Mismatches 99; Indels 23; Gaps
                                                                 8;
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
Qу
            2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
Db
         90 GES-VEPEPEADYYAKEVTRVLMVESGNO1YDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
             62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
Db
        149 LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
            121 LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
Db
        204 VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
Qу
            181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEO-ORGDMOSIAKKHRRVPYV 239
Db
        259 LLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFRKDLGW 316
Qу
            Db
        240 LAMALPAERANELHSARRRD------LDTDYCFGPGTDEKNCCVRPLYIDFRKDLQW 291
```

CC

```
Qу
         317 KWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALEPLPIVY 376
             Db
         292 KWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDPLPIIY 351
Ov
         377 YVGRKPKVEQLSNMIVRSCKCS 398
             Db
         352 YVGRNVRVEQLSNMVVRACKCS 373
RESULT 12
TGF1 XENLA
    TGF1 XENLA
                  STANDARD;
                              PRT; 382 AA.
AC
    P16176:
    01-APR-1990 (Rel. 14, Created)
DT
    01-APR-1990 (Rel. 14, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 5).
DE
OS
    Xenopus laevis (African clawed frog).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC
OC
    Xenopodinae; Xenopus.
OX
    NCBI TaxID=8355;
RN
    [1]
RP
    SEOUENCE FROM N.A.
RX
    MEDLINE=90110090; PubMed=2295601;
RA
    Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B.,
RA
    Sporn M.B., Melton D.A.;
RT
    "Identification of a novel transforming growth factor-beta (TGF-beta
RT
    5) mRNA in Xenopus laevis.";
RL
    J. Biol. Chem. 265:1089-1093(1990).
RN
    [2]
RP
    SEQUENCE FROM N.A.
RA
    Vempati U.D., Kondaiah P.;
RL
    Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; J05180; AAA49968.1; -.
DR
    EMBL; AF009335; AAB64441.1; -.
DR
    EMBL; AF009331; AAB64441.1; JOINED.
    EMBL; AF009332; AAB64441.1; JOINED.
DR
    EMBL; AF009333; AAB64441.1; JOINED.
DR
DR
    EMBL; AF009334; AAB64441.1; JOINED.
DR
    PIR; A34929; B61036.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
```

```
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                      21
                              POTENTIAL.
FT
    PROPEP
               22
                     270
FT
    CHAIN
               271
                     382
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
               277
                     286
                              BY SIMILARITY.
FT
    DISULFID
               285
                     348
                              BY SIMILARITY.
FΤ
    DISULFID
               314
                     379
                              BY SIMILARITY.
FT
    DISULFID
               318
                     381
                              BY SIMILARITY.
FT
    DISULFID
               347
                     347
                              INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
               73
                     73
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
               123
                     123
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
              166
                     166
FT
    SITE
                             CELL ATTACHMENT SITE (POTENTIAL).
               234
                     236
SO
    SEOUENCE
              382 AA; 44200 MW; 1034621C917AAE15 CRC64;
 Query Match
                       41.3%; Score 873; DB 1; Length 382;
 Best Local Similarity 46.9%; Pred. No. 9.2e-62;
 Matches 190; Conservative 55; Mismatches 122; Indels 38; Gaps
                                                                   11:
          9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
Qу
            : :| || || || ||
                          Db
          1 MEVLWMLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS 59
         69 PPGPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDK 123
Qу
                  : ||||| : : :: |
                                         Db
         60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
        124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW-- 179
Qу
                      116 ----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKOTDKNMDORMELFWKYOENGTTH 170
Db
        180 -RYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
Qу
             : :||
        171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
Db
        236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYC 293
Qу
                               Db
        227 IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR-----GVGQEYC 277
        294 FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ 353
Qу
                 278 FGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQYSKVLSLYNQ 337
Db
        354 HNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            338 NNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382
Db
```

```
RESULT 13
TGF3 CHICK
ID
    TGF3 CHICK
                   STANDARD;
                                  PRT;
                                       412 AA.
AC
    P16047:
DT
    01-APR-1990 (Rel. 14, Created)
DT
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
    TGFB3.
OS
    Gallus gallus (Chicken).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC
    Gallus.
OX
    NCBI TaxID=9031;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=89096966; PubMed=3211158;
RA
    Jakowlew S.B., Dillard P.J., Kondaiah P., Sporn M.B., Roberts A.B.;
    "Complementary deoxyribonucleic acid cloning of a novel transforming
RT
RT
    growth factor-beta messenger ribonucleic acid from chick embryo
RT
    chondrocytes.";
    Mol. Endocrinol. 2:747-755(1988).
RL
RN
    [2]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=White leghorn:
RX
    MEDLINE=95169270; PubMed=7865129;
RA
    Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;
    "The chicken transforming growth factor-beta 3 gene: genomic
RT
RT
    structure, transcriptional analysis, and chromosomal location.";
RL
    DNA Cell Biol. 14:111-123(1995).
RN
RP
    SEQUENCE OF 1-117 FROM N.A.
RC
    STRAIN=White leghorn; TISSUE=Blood;
RX
    MEDLINE=92134496; PubMed=1840616;
RA
    Burt D.W., Dey B.R., Paton I.R.;
RT
    "Comparative analysis of human and chicken transforming growth
RT
    factor-beta 2 and -beta 3 promoters.";
RL
    J. Mol. Endocrinol. 7:175-183(1991).
RN
    [4]
    SEQUENCE OF 1-117 FROM N.A.
RP
RX
    MEDLINE=93024487: PubMed=1406706:
RA
    Jakowlew S.B., Lechleider R., Geiser A.G., Kim S.J.,
    Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
RA
RT
    "Identification and characterization of the chicken transforming
RT
    growth factor-beta 3 promoter.";
RL
    Mol. Endocrinol. 6:1285-1298(1992).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC
    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; M31154; AAA49089.1; -.
DR
    EMBL; X58127; CAA41128.2; -.
    EMBL; X60055; CAA41128.2; JOINED.
DR
    EMBL; X60091; CAA41128.2; JOINED.
DR
    EMBL; X60090; CAA41128.2; JOINED.
DR
DR
    EMBL; S46000; AAB23575.1; -.
DR
    PIR; A34939; A34939.
    HSSP; P10600; 1TGJ.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
               1
                     23
                            POTENTIAL.
FT
    PROPEP
               24
                     300
FT
    CHAIN
              301
                    412
                             TRANSFORMING GROWTH FACTOR BETA 3.
FT
    DISULFID
             307 316
                            BY SIMILARITY.
FT
    DISULFID
             315 378
                            BY SIMILARITY.
             344 409
                            BY SIMILARITY.
FT
    DISULFID
                            BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
    DISULFID 348 411
FT
    DISULFID 377 377
CARBOHYD 74 74
CARBOHYD 135 135
FT
FT
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD 142 142
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
                            CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
             261 263
FT
                            ELPT -> DFRQ (IN REF. 1).
    CONFLICT
              323 326
    SEQUENCE 412 AA; 47077 MW; 1CAB883170069D55 CRC64;
SQ
 Query Match
                      40.5%; Score 857; DB 1; Length 412;
 Best Local Similarity 46.4%; Pred. No. 1.9e-60;
 Matches 195; Conservative 56; Mismatches 117; Indels 52; Gaps
Qy
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSOGDVPPGPLP 74
            9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66
Db
         75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNOIYDKF 124
Qу
              :|||||||||||: ||:|||||: ||:: ||:: ||:: ||::
         67 YQILALYNSTRELL--EEMEEEKEESCSQENTESEYYAKEIHKFDMIOGLPEHNELGICP 124
Db
Qу
         125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
            Db
        125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180
        178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
Qу
               181 AKQRYLSGRNVQTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240
Db
```

```
Qу
        230 N---TLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAOH--LHSSRHRR 278
            1
               Db
        241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300
        279 DYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIW 338
Qу
                   301 -----ALDTNYCFRNLEENCCVRPLYIELPTDLGWKWVHEPKGYFANFCSGPCPYLR 352
Db
Qу
        339 SLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Dh
        353 SADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
RESULT 14
TGF3 PIG
ID
    TGF3 PIG
                 STANDARD;
                             PRT; 409 AA.
AC
    P15203;
DT
    01-APR-1990 (Rel. 14, Created)
DT
    01-APR-1990 (Rel. 14, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
    TGFB3.
OS
    Sus scrofa (Pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC
OX
    NCBI TaxID=9823;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Ovary;
RX
    MEDLINE=89091120; PubMed=3208746;
RA
    Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L.,
RA
    Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
RA
    Chen E.Y.;
RT
    "A new type of transforming growth factor-beta, TGF-beta 3.";
RL
    EMBO J. 7:3737-3743(1988).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
    ______
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
CC
    -----
DR
    EMBL; X14150; CAA32363.1; -.
DR
    PIR; S01825; S01825.
    HSSP; P10600; 1TGJ.
DR
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
```

```
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                      18
                               POTENTIAL.
FT
    PROPEP
                19
                     297
FT
    CHAIN
               298
                     409
                              TRANSFORMING GROWTH FACTOR BETA 3.
FT
    DISULFID
               304
                     313
                               BY SIMILARITY.
FT
    DISULFID
                     375
                               BY SIMILARITY.
               312
FT
    DISULFID
               341
                     406
                              BY SIMILARITY.
FT
    DISULFID
               345
                     408
                               BY SIMILARITY.
                               INTERCHAIN (BY SIMILARITY).
FT
    DISULFID
               374
                     374
FT
    CARBOHYD
               72
                      72
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               133
                     133
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               140
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                     140
                              CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
               259
                     261
              409 AA; 46814 MW; B4900235B5CC955E CRC64;
SQ
    SEQUENCE
 Query Match 39.7%; Score 838.5; DB 1; Length 409; Best Local Similarity 45.6%; Pred. No. 5.4e-59;
 Matches 190; Conservative 58; Mismatches 122; Indels
                                                          47: Gaps
                                                                     14:
          15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
            7 LVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGQILSKLRLTSPPDPSML--ANIP 64
Db
          75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNOIYDKFKG 126
Qу
              -:||| : : |::|||||::||
Db
          65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
Qу
                                 ] | | | | | : | | :
                                                : || :||:|
                :: || | : :
         125 ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
Db
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             : 1 :1
         181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
Db
         231 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAOH--LHSSRHRRDYK 281
Qу
               : :: | :|
                            241 QEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAQRKKR--- 297
Db
         282 DDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD 341
Qу
                 Db
         298 ----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSAD 352
Qу
         342 TOYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         353 TTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTAKVEQLSNMVVKSCKCS 409
RESULT 15
TGF3 MOUSE
ID
    TGF3 MOUSE
                  STANDARD;
                               PRT;
                                      410 AA.
AC
    P17125;
```

```
01-AUG-1990 (Rel. 15, Created)
DT
DT
    01-AUG-1990 (Rel. 15, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 3 precursor (TGF-beta 3).
DE
GN
    TGFB3.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=90190650; PubMed=2628730;
RA
    Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RT
     "Complementary DNA cloning of the murine transforming growth
RT
    factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT
    of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT
    adult tissues.";
    Mol. Endocrinol. 3:1926-1934(1989).
RL
RN
    [2]
RP
    SEQUENCE FROM N.A.
    MEDLINE=91000714; PubMed=2206556;
RX
    Denhez F., Lafyatis R., Kondaiah P., Roberts A.B., Sporn M.B.;
RA
    "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT
RT
    mTGF-beta 3.";
RL
    Growth Factors 3:139-146(1990).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
CC
     ______
CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
CC
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
     -----
DR
    EMBL; M32745; AAA40422.1; -.
DR
    PIR; A41397; A41397.
DR
    HSSP: P10600; 1TGJ.
DR
    MGD; MGI:98727; Tqfb3.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb_N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
                1 23
    SIGNAL
                              POTENTIAL.
    PROPEP
                       298
FT
                 24
                                POTENTIAL.
FT
    CHAIN
                299
                      410
                               TRANSFORMING GROWTH FACTOR BETA 3.
```

```
FT
    DISULFID
              305
                    314
                            BY SIMILARITY.
FT
    DISULFID
              313
                    376
                            BY SIMILARITY.
FT
    DISULFID
                    407
              342
                            BY SIMILARITY.
FT
    DISULFID
                    409
              346
                            BY SIMILARITY.
FT
    DISULFID
              375
                    375
                            INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
              72
                    72
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
              133
                    133
FT
    CARBOHYD
              140
                    140
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
              259
                    261
                            CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE
             410 AA; 46884 MW; 250F7048CA432BD6 CRC64;
 Query Match
                     39.5%; Score 835; DB 1; Length 410;
 Best Local Similarity 45.2%; Pred. No. 1e-58;
 Matches 188; Conservative 58; Mismatches 126; Indels 44; Gaps
                                                                13;
Qу
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
            Db
          7 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP 64
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG 126
Qу
             Db
         65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
        127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEOHVELYOKYSND----S 178
Qу
               :: || | : :
                              __ : || :||:|
        125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
Db
        179 WRYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             Db
        181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFOPNGDILENV 240
        231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRDYKD 282
Qу
              : :: | ::
                           Db
        241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGOGSORK---- 296
        283 DDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342
Qу
              Db
        297 -- KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADT 354
        343 QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
        355 THSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 410
```

Search completed: October 28, 2003, 09:08:38 Job time: 9.97725 secs

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 07:50:55; Search time 31.909 Seconds (without alignments) 3218.683 Million cell updates/sec

Title: US-10-017-372E-9

Perfect score: 2114

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
4: sp human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

٥.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		र्ड				
Result		Query				
No.	Score	Match :	Length	DB	ID	Description
1	1820	86.1	390	6	 09TUM8	Q9tum8 equus cabal
2	1741	82.4	368	11	Q8R4D9	Q8r4d9 sigmodon hi
3	848	40.1	379	13	Q8JHF5	Q8jhf5 sparus aura
4	844	39.9	379	13	Q8AXK8	Q8axk8 sparus aura
5	835	39.5	412	11	Q91YU7	Q91yu7 mus musculu
6	828.5	39.2	414	11	Q91VP5	Q91vp5 mus musculu
7	824.5	39.0	382	13	Q9PWA9	Q9pwa9 morone chry
8	808.5	38.2	382	13	093449	093449 oncorhynchu
9	782.5	37.0	376	13	Q9PTQ2	Q9ptq2 cyprinus ca
10	767.5	36.3	399	11	Q9ERB7	Q9erb7 mesocricetu
11	727	34.4	362	11	Q99K17	Q99k17 mus musculu

```
130 11 Q08714
12
      696
           32.9
                                                   008714 mesocricetu
13
      681
           32.2
                   361 13 098854
                                                   Q98854 cyprinus ca
14
      679
           32.1
                  124 6 O95N80
                                                  Q95n80 canis famil
15
      638
           30.2
                  112 6 002730
                                                  002730 oryctolagus
16
    607.5
           28.7
                   255 11 0921T1
                                                   Q921t1 mus musculu
           27.9
17
      589
                127 6 O9TV08
                                                  Q9tv08 canis famil
                  224 11 Q8CDZ9
18
    577.5
           27.3
                                                   O8cdz9 mus musculu
                  200 13 Q90YF1
19
     557
           26.3
                                                   090yf1 pleuronecte
           26.2
20
      554
                  101 11 Q9R184
                                                   Q9r184 meriones un
21
   463.5
          21.9 179 13 Q90YF2
                                                   Q90yf2 pleuronecte
          19.5
22
     413
                  88 13 Q90YF5
                                                   Q90yf5 pleuronecte
23
      402
          19.0
                  88 13 Q90YF7
                                                   Q90yf7 oncorhynchu
                  88 13 Q90ZE7
24
      397
           18.8
                                                  Q90ze7 acipenser b
                  87 13 042306
25
      393
           18.6
                                                  042306 carassius a
           18.1
17.9
                   91 6 O9MYZ1
26
      383
                                                  Q9myzl capra hircu
                   309 4 Q8WV88
                                                  Q8wv88 homo sapien
27
      379
      373
28
           17.6 86 6 Q28241
                                                  Q28241 cervus elap
29
      358
           16.9
                   81 6 Q9N1S3
                                                  Q9n1s3 capreolus c
30
      352
           16.7
                   375 13 Q8UWD8
                                                  Q8uwd8 columba liv
31
      339
          16.0
                  375 13 Q8AVB2
                                                   O8avb2 coturnix co
32
      337
           15.9
                  375 13 Q8UWD7
                                                   Q8uwd7 coturnix ch
                   375 13 Q98SP0
33
      332
           15.7
                                                  Q98sp0 gallus gall
34
      329
           15.6
                   375 6 Q9GM97
                                                  Q9gm97 equus cabal
35
      329
           15.6
                   375 13 Q8UWE0
                                                   Q8uwe0 anas platyr
36
           15.6
      329
                  389 13 Q90YY0
                                                   Q90yy0 ictalurus p
37
     327
          15.5 375 13 Q8UWD9
                                                   O8uwd9 anser anser
38
     325
          15.4 375 6 Q8HY52
                                                  O8hy52 lepus capen
          15.2 375 6 Q95J86
39
     322
                                                Q95j86 macaca fasc
                  87 13 Q8JHB6
40
      320
          15.1
                                                  Q8jhb6 scophthalmu
                   77 13 O90YF8
41
      317
          15.0
                                                  Q90yf8 oncorhynchu
42
      312
           14.8
                   375
                       6 Q8WNS6
                                                  08wns6 bos taurus
43
    307.5
          14.5
                   376 13 Q98TB4
                                                  Q98tb4 oreochromis
44
    306.5
          14.5
                   376 13 Q90W06
                                                   Q90w06 umbrina cir
45
    303.5 14.4
                   385 13 Q90W05
                                                   Q90w05 sparus aura
```

ALIGNMENTS

```
RESULT 1
Q9TUM8
ID
     Q9TUM8
                 PRELIMINARY;
                                    PRT;
                                           390 AA.
AC
     O9TUM8;
DT
     01-MAY-2000 (TrEMBLrel. 13, Created)
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
     Transforming growth factor beta 1.
GN
     TGFB1.
ĊS
     Equus caballus (Horse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX
    NCBI TaxID=9796;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RA
     Nixon A.J., Brower-Toland B.T., Sandell L.J.;
RT
     "Molecular cloning of equine transforming growth factor beta 1 reveals
RT
     a divergent nucleotide structure that encodes a novel bioactive
```

```
RT
    peptide among mammalian species.";
RL
    Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL: AF175709: AAD49431.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb_N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
SO
    SEOUENCE
             390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;
 Query Match
                      86.1%; Score 1820; DB 6; Length 390;
                     87.4%; Pred. No. 6.5e-154;
 Best Local Similarity
 Matches 348; Conservative 12; Mismatches
                                         30; Indels
                                                      8; Gaps
                                                                 1;
Oy
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI 120
Db
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                  121 YKTVETGSHSIYMFFNASELRAAVPDPMLLSRAELRLLRLKLSVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGLRLSAHCPCDSKDNTLRVGINGFS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKN 300
Qу
            241 SSRRGDLATIDGMNRPFLLLMATPLERAOOLHSSRHRR-----ALDTNYCSSSTEKN 292
Dh
        301 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 360
Qу
            Db
        293 CCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASA 352
        361 APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            ďu
        353 APCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 2
08R4D9
ΙD
    Q8R4D9
              PRELIMINARY;
                             PRT:
                                   368 AA.
AC
    Q8R4D9;
DT
    01-JUN-2002 (TrEMBLrel. 21, Created)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
```

```
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta-1 protein (Fragment).
GN
OS
    Sigmodon hispidus (Hispid cotton rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC
    Sigmodon.
OX
    NCBI_TaxID=42415;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Blanco J.C., Pletneva L.M., Prince G.A.;
RT
    "Cotton rat cytokines, chemokines, and interferons.";
RL
    Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
DR
    EMBL; AF480858; AAL87199.1; -.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
FT
    NON TER
                1
                     1
SO
    SEOUENCE
             368 AA; 41905 MW; A5C91207B0468B4A CRC64;
 Query Match
                      82.4%; Score 1741; DB 11; Length 368;
 Best Local Similarity 86.4%; Pred. No. 6.7e-147;
 Matches 325; Conservative 16; Mismatches
                                           27; Indels
                                                        8; Gaps
                                                                  1;
         23 PGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYN 82
Qу
            1 PGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYN 60
Db
         83 STRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELRE 142
Qу
            61 STRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYDKTKDIPHSVYMFFNTSDIRE 120
Db
        143 AVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTG 202
Qу
            121 AVPEPPLLSRAELRLQRFKSNVEQHVELYEKYSNNSWRYLGNRLLSPTDSPEWLSFDVTS 180
Db
Qу
        203 VVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMA 262
            Db
        181 VVRKWLNQGDGIQGFRFSAHCSCDSKDNILHVEINGISPKRRGDLGTIHDMNRPFLLLMA 240
        263 TPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEP 322
Qу
            Db
        241 TPLERAQHLHSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEP 292
        323 KGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKP 382
Qу
            293 KGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKP 352
Db
        383 KVEQLSNMIVRSCKCS 398
Qу
            1111111111
```

```
RESULT 3
O8JHF5
ΙD
    Q8JHF5
                PRELIMINARY;
                                 PRT;
                                       379 AA.
AC
    Q8JHF5;
DT
    01-OCT-2002 (TrEMBLrel. 22, Created)
DT
    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta 1.
OS
    Sparus aurata (Gilthead sea bream).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
    Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC
    Sparidae; Sparus.
OX
    NCBI_TaxID=8175;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Tafalla C., Aranguren R., Secombes C.J., Castrillo J.L., Novoa B.,
    Figueras A.;
RA
RT
    "Molecular characterization of sea bream (Sparus aurata) transforming
RT
    growth factor betal.";
RI.
    Fish and Shellfish Immunol. 0:0-0(2002).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF510084; AAN03842.1; -.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 2.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA_1; 1.
DR
SQ
    SEQUENCE 379 AA; 43506 MW; COC9D3D2FCA29C0E CRC64;
 Query Match
                        40.1%; Score 848; DB 13; Length 379;
 Best Local Similarity
                        46.5%; Pred. No. 3.5e-67;
 Matches 186; Conservative 68; Mismatches 110; Indels
                                                            36; Gaps
Qу
          12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL-ASPPSQGDVPP 70
             Db
           3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPTESPQAGD--E 59
          71 GPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDKFK 125
Qу
               : | :|:|
                                                     111
Db
          60 EEIPSSLLSLYNSTKEMLKEQQTEVQTDIFTEQEEEEYFA---TRVHKFNTTNPV----- 111
Qу
         126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV---EQHVELYQKYSNDSWRYL 182
              \\ :: \ \\ \\\:\:\: :\\:\\:\\\:\\\:\\
                                                    112 RTPQNMSMSFNISEIRRSIGDYRLLTTAELRML-IKAPTILDEQRVELYQGLGT-SPRYL 169
Db
Qу
         183 SNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTLHVEINGFN 240
             :: :
```

```
Db
         170 ASRFITNELRDKWLSFDVTETLQNWLKGNDDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229
Qу
         241 SGRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTE 298
            230 AG-RGDKAVLDDMTKOPPYILTMSIPKNVSSHL-TSRKKRSTETKDT-----CTAOTE 280
Db
         299 KNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGA 358
Qу
              281 -TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNAENKYSOILALYKHHNPGA 339
Db
         359 SAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
Qу
            Db
         340 SAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 379
RESULT 4
Q8AXK8
ID
    O8AXK8
               PRELIMINARY;
                               PRT:
                                     379 AA.
AC
    Q8AXK8;
DT
    01-MAR-2003 (TrEMBLrel. 23, Created)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta 1.
OS
    Sparus aurata (Gilthead sea bream).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
    Acanthomorpha; Acanthopteryqii; Percomorpha; Perciformes: Percoidei:
OC
    Sparidae; Sparus.
OX
    NCBI TaxID=8175;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Tafalla C., Novoa B., Aranguren R., Figueras A.;
RT
    "Molecular cloning and characterization of sea bream (Sparus aurata)
RT
    TGF beta 1.";
RL
    Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF424703; AAN76665.1; -.
    SEQUENCE 379 AA; 43485 MW; A306EC387F6DBA7C CRC64;
SQ
 Query Match
                       39.9%; Score 844; DB 13; Length 379;
 Best Local Similarity
                       46.5%; Pred. No. 8.1e-67;
 Matches 186; Conservative 67; Mismatches 111; Indels
                                                        36: Gaps
                                                                   15:
         12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL-ASPPSQGDVPP 70
Qу
            Db
          3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPTESPQAGD--E 59
         71 GPLPEAVLALYNSTRDRVAGESVEPEPE----PEADYYAKEVTRVLMVESGNQIYDKFK 125
Qу
              : | :
ďU
         60 EEIPSSLLSLYNSTKEMLKEQQTEVQTDIFTEXEEEEYFA---TRVHKFNTTNPV----- 111
        126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV---EQHVELYQKYSNDSWRYL 182
Qу
             Db
        112 RTPQNMSMSFNISEIRRSIGDYRLLTTAELRML-IKAPTILDEQRVELYQGLGT-SPRYL 169
Qу
        183 SNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTLHVEINGFN 240
            :: :
                      :|||||| :: || :: || ||
                                                    | :|
Db
        170 ASRFITNELRDKWLSFDVTETLQNWLKGNDDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229
```

```
Qу
                   241 SGRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTE 298
                           :| | | | | : | : | : | : | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                Db
                   230 AG-RGDKAVLDDMTKQPPYILTMSIPKNVSSHL-TSRKKRSTETKDT-----CTAQTE 280
                   299 KNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGA 358
ОУ
                               Db
                   281 -TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNAENKYSOXLALYKHHNPGA 339
                   359 SAAPCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 398
Qу
                           Db
                   340 SAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 379
RESULT 5
Q91YU7
ID
         Q91YU7
                                PRELIMINARY;
                                                               PRT;
                                                                               412 AA.
AC
         Q91YU7;
DT
         01-DEC-2001 (TrEMBLrel. 19, Created)
DT
         01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
         01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
         Transforming growth factor, beta 3.
GN
         TGFB3.
OS
         Mus musculus (Mouse).
OC
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
         NCBI TaxID=10090;
RN
         [1]
RP
         SEQUENCE FROM N.A.
RA
         Strausberg R.;
RL
         Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
         -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
         EMBL; BC014690; AAH14690.1; -.
DR
DR
         MGD; MGI:98727; Tgfb3.
         InterPro; IPR002400; GF_cysknot.
DR
DR
         InterPro; IPR001839; TGFb.
         InterPro; IPR001111; TGFb N.
DR
         InterPro; IPR003911; TGF_TGFb.
DR
DR
         Pfam; PF00019; TGF-beta; 1.
DR
         Pfam; PF00688; TGFb propeptide; 1.
DR
         PRINTS; PR00438; GFCYSKNOT.
DR
         PRINTS; PR01423; TGFBETA.
DR
         ProDom; PD000357; TGFb; 1.
DR
         SMART; SM00204; TGFB; 1.
DR
         PROSITE; PS00250; TGF BETA 1; 1.
SQ
         SEQUENCE 412 AA; 47144 MW; F3EB65D046DF32AD CRC64;
   Query Match
                                                 39.5%; Score 835; DB 11; Length 412;
   Best Local Similarity 45.2%; Pred. No. 5.8e-66;
   Matches 188; Conservative 58; Mismatches 126; Indels 44; Gaps
                                                                                                                                                13;
Qу
                     15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                                             Db
                      9 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGOILSKLRLTSPPEPSVMT--HVP 66
                    75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG 126
Qу
```

```
Db
         67 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 126
Qу
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYOKYSND----S 178
                :: [] [:::
                                             : || :||:|
                                 Db
         127 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFOILRPDEHIAK 182
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             Db
         183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFOPNGDILENV 242
         231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRDYKD 282
Qу
               Db
         243 HEVMEIKFKGVDNEDDHGRGDLGRLKKOKDHHNPHLILMMIPPHRLDSPGOGSORK---- 298
         283 DDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT 342
Qу
               299 -- KRALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADT 356
Db
Qу
         343 QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         357 THSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
RESULT 6
091VP5
               PRELIMINARY;
                              PRT;
                                     414 AA.
ID
    Q91VP5
AC
    Q91VP5;
    01-DEC-2001 (TrEMBLrel. 19, Created)
DT
DT
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
    Similar to transforming growth factor, beta 2.
GN
    TGFB2.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Breast tumor;
RA
    Strausberg R.;
    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RL
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; BC011170; AAH11170.1; -.
    MGD; MGI:98726; Tqfb2.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
DR
    Ptam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA 1; 1.
SQ
    SEQUENCE 414 AA; 47588 MW; DB37A7C38881F286 CRC64;
```

```
Query Match 39.2%; Score 828.5; DB 11; Length 414; Best Local Similarity 44.2%; Pred. No. 2.2e-65;
 Matches 188; Conservative 63; Mismatches 121; Indels 53; Gaps
                                                                  15:
         12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSOGDVP-P 70
Qу
                 Db
          5 VLSTFLLLHLVP--VALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEP 60
         71 GPLPEAVLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNOIYD 122
Qу
              Db
         61 DEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHLPSENAIPP 120
        123 KFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----K 173
Qу
             121 TFY-RPYFRIVRFDVSTMEKNASN---LVKAEFRVFRLQNPKARVAEQRIELYQILKSKD 176
Dh
        174 YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSS----- 225
Qу
             :: : ||: ::::
                             177 LTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVQEWLHHKDRNLGFKISLHCPCCTFVPSNN 236
Dh
        226 ---DSKDNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHS 273
Qу
                         Db
        237 YIIPNKSEELEARFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHLLLMLLPSYRLESQQS 296
        274 SRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 333
Qу
                      297 SRRKK------RALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGA 349
Db
        334 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 393
Qу
            Db
        350 CPYLWSSDTQHTKVLSLYNTINPEASASPCCVSQDLEPLTILYYIGNTPKIEQLSNMIVK 409
Qу
        394 SCKCS 398
            Db
        410 SCKCS 414
RESULT 7
Q9PWA9
ID
    Q9PWA9
              PRELIMINARY;
                              PRT;
                                    382 AA.
AC
    Q9PWA9;
DT
    01-MAY-2000 (TrEMBLrel. 13, Created)
DT
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta precursor.
GN
    TGF-BETA.
OS
    Morone chrysops x Morone saxatilis (white bass x striped bass).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ОC
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
    Acanthomorpha; Acanthopteryqii; Percomorpha; Perciformes; Percoidei;
OC
    Moronidae; Morone.
    NCBI TaxID=45352;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC
    TISSUE=KIDNEY;
ВX
    MEDLINE=20394636; PubMed=10938723;
RA
    Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
```

```
RT
     "Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
RT
    chrysops) transforming growth factor-beta (TGF-beta), and development
RT
    of a reverse transcription quantitative competitive polymerase chain
RT
    reaction (RT-qcPCR) assay to measure TGF-beta mRNA of teleost fish.";
RL
    Fish Shellfish Immunol. 10:61-85(2000).
     -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
     -!- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
CC
        PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
CC
     -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
     EMBL; AF140363; AAD46997.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR001839; TGFb.
DR
DR
     InterPro; IPR001111; TGFb_N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                 1
                        っ
                                POTENTIAL.
FT
                 ?
    PROPEP
                      270
FT
    CHAIN
                271
                      382
                                TRANSFORMING GROWTH FACTOR BETA.
FT
    DISULFID
                278
                      286
                               BY SIMILARITY.
FT
                               BY SIMILARITY.
    DISULFID
                285
                      348
FT
    DISULFID
                314
                      379
                               BY SIMILARITY.
FT
    DISULFID
             318
                      381
                               BY SIMILARITY.
FT
    DISULFID
             347 347
                                INTERCHAIN (BY SIMILARITY).
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                73
                      73
FT
    CARBOHYD
               108
                      108
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
                                N-LINKED (GLCNAC. . .) (POTENTIAL) .
    CARBOHYD
               113
                      113
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               124
                      124
FT
    CARBOHYD
               259
                      259
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
               235
                      237
                               CELL ATTACHMENT SITE (POTENTIAL).
    SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;
SO
 Query Match
                        39.0%; Score 824.5; DB 13; Length 382;
 Best Local Similarity 46.1%; Pred. No. 4.5e-65;
 Matches 184; Conservative 64; Mismatches 114; Indels
                                                            37: Gaps
                                                                        14:
Qу
          15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL---ASPPSQGDVPPG 71
             ďŪ
           6 LMLVVVYTVGN-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPKEPEPDQAGDEEEI 64
          72 PLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDKFKG 126
Qу
             Db
          65 PTP--LLSLYNSTKEMLKEQQTEVQTDISTEQEEEEYFAKVLHKFNMTRKNN----- 114
Qу
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV--EQHVELYQKYSNDSWRYLSN 184
              Db
         115 TDTTKKMFFNISEIRESVGDYRLLTSAELRMLIKKTTIYDEQRVELYSGL-GDSPRYLAS 173
```

RA

Tompkins W.A.F.;

```
185 RLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTL-HVEINGFNS 241
Qу
                      :|||||||
                                                  : | |:
         174 RFITNKWKDKWLSFDVTKTLQDWLKGTDDEQGFQLRLFCECNKVSAGETIFKFGISGIDP 233
Dh
         242 GRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEK 299
Qу
                    : | : ||
Db
         234 G-RGDTGPMQLLTQQPPYILTMSIP----QNISSPSTSRKKRSTETK----DVCTAQTE- 283
Qу
         300 NCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS 359
              Db
         284 TCCVRSLYIDFRKDLGWKWIHKPTGYNANYCMGSCTYIWNAENKYSOILALYKHHNPGAS 343
Qу
         360 AAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         344 AQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 382
RESULT 8
093449
ΙD
    093449
                PRELIMINARY;
                                PRT; 382 AA.
AC
    093449; Q91217;
    01-NOV-1998 (TrEMBLrel. 08, Created)
DT
DT
    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta precursor.
GN
    TGF-BETA OR TGF.
OS
    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC
    Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX
    NCBI TaxID=8022;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=LEUKOCYTE;
RX
    MEDLINE=99242020; PubMed=10227481;
RA
    Daniels G.D., Secombes C.J.;
RT
    "Genomic organisation of rainbow trout, Oncorhynchus mykiss TGF-
RT
    BETA.";
RL
    Dev. Comp. Immunol. 23:139-147(1999).
RN
RΡ
    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC
    TISSUE=LEUKOCYTE;
    MEDLINE=98390168; PubMed=9722928;
RX
RA
    Hardie L.J., Laing K.J., Daniels G.D., Grabowski P.S., Cunningham C.,
    Secombes C.J.;
RA
RT
    "Isolation of the first piscine transforming growth factor beta gene:
    analysis reveals tissue specific expression and a potential regulatory
RT
    sequence in rainbow trout (Oncorhynchus mykiss).";
RT
RL
    Cytokine 10:555-563(1998).
CC
    -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- TISSUE SPECIFICITY: EXPRESSED IN BLOOD LEUKOCYTES, KIDNEY
CC
        MACROPHAGES, BRAIN, GILL AND SPLEEN BUT NOT IN LIVER.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
    EMBL; AJ007836; CAA07707.1; -.
```

```
DR
    EMBL; X99303; CAA67685.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                     20
                             POTENTIAL.
               1
FT
    PROPEP
                     270
               21
FT
    CHAIN
               271
                     382
                             TRANSFORMING GROWTH FACTOR BETA.
                             BY SIMILARITY.
FT
    DISULFID
               278
                     286
FT
    DISULFID
               285
                     348
                            BY SIMILARITY.
FT
    DISULFID
              314
                    379
                            BY SIMILARITY.
FT
    DISULFID 318
                    381
                             BY SIMILARITY.
                             INTERCHAIN (BY SIMILARITY).
FT
    DISULFID 347 347
    CARBOHYD
                     76
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
               76
    CARBOHYD
FT
              116
                    116
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD 125 125
FT
    CONFLICT 237 237
                            N \rightarrow D (IN REF. 2).
FT
    CONFLICT 345 345
                             Q \rightarrow H (IN REF. 2).
FT
    CONFLICT
             371
                    372
                             LS -> VP (IN REF. 2).
FT
    CONFLICT 377
                    377
                            K \rightarrow M (IN REF. 2).
              382 AA; 44136 MW; 93BD4D3540084B92 CRC64;
SO
    SEQUENCE
 Query Match
                      38.2%; Score 808.5; DB 13; Length 382;
 Best Local Similarity 47.1%; Pred. No. 1.2e-63;
 Matches 181; Conservative 57; Mismatches 107; Indels
                                                        39; Gaps
                                                                   13;
Qу
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPP---SQGDVPPGPLPEAVLALYNSTRD 86
            Db
         23 MSTCKSLDLELVKRKRIEAIRGQILSKLRLPKEPEIDQEGDTE--EVPASLMSIYNSTVE 80
Qу
         87 RVAGESVE-----PEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSEL 140
             Db
         81 -LSEEQVHTYIPSTQDAEEEA-YFAKEVHKFNMKQSENT-----SKHQI--LFNMSEM 129
         141 REAVPEPVLLSRAELRLL----RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWL 196
Qу
            Db
         130 RSVLGTDRLLSQAELRLLIKNHGLLDDSEQRLELYRGV-GDKARYLKSHFVSKEWANRWV 188
         197 SFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATI -- HGMN 254
Qу
                            : []: [
            : | : | |
                                                    ||: |:
Db
        189 SFDVTQTLNEWLQGAGEEQGFQLKLPCDCGKPMEEFRFKISGMNK-LRGNTETLAMKMPS 247
Qу
        255 RPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDL 314
            : 1 : 1 1 1 : 1 : 1 1 1 1 1 1 1 1 1 1
                                        Db
        248 KPHILLMSLPVERHSQL-SSRKKRQ-----TTTEEICSDKSESCCVRKLYIDFRKDL 298
Qу
        315 GWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPI 374
```

```
Db
         299 GWKWIHEPTGYFANYCIGPCTYIWNTENKYSQVLALYKHHNPGASAQPCCVPQVLEPLPI 358
Qу
         375 VYYVGRKPKVEQLSNMIVRSCKCS 398
             Db
         359 IYYVGROHKVEQLSNMIVKSCRCS 382
RESULT 9
Q9PTQ2
ΙD
    Q9PTQ2
                PRELIMINARY;
                                  PRT:
                                         376 AA.
AC
    O9PTQ2;
DT
    01-MAY-2000 (TrEMBLrel. 13, Created)
DT
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta precursor.
OS
    Cyprinus carpio (Common carp).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC
    Cyprinidae; Cyprinus.
OX
    NCBI TaxID=7962;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Yin Z., Kuang J.;
     "Molecular cloning of carp transforming growth factor beta 1.";
RT
RL
    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
    -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF136947; AAF22573.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
    SIGNAL
                        22
                                 POTENTIAL.
                  1
FT
    PROPEP
                 23
                       264
FT
                       376
                                 TRANSFORMING GROWTH FACTOR BETA.
    CHAIN
                265
                       280
                                 BY SIMILARITY.
FT
    DISULFID
                272
FT
                308
                       373
                                 BY SIMILARITY.
    DISULFID
FT
    DISULFID
                312
                       375
                                BY SIMILARITY.
FΤ
              341
                      341
                                 INTERCHAIN (BY SIMILARITY).
    DISULFID
FT
    CARBOHYD
                76
                       76
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               125
                      125
               167
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                      167
FT
    SITE
                230
                       232
                                CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE
               376 AA; 43329 MW; 7F7FC4DA58B69681 CRC64;
 Query Match
                         37.0%; Score 782.5; DB 13; Length 376;
 Best Local Similarity 44.5%; Pred. No. 2.5e-61;
 Matches 179; Conservative 67; Mismatches 119; Indels 37; Gaps
```

```
Qу
           6 LRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSO 65
                           1 MRVESLLLALQCLLGFV--HYSGALSTCSPLDLELIKRKRIEAIRGQILSKLRLSKEPEV 58
Db
          66 GDVPPGP-LPEAVLALYNST---RDRVAGESVEPEPEP-EADYYAKEVTR--VLMVESGN 118
Qу
                   :| ::::||| : | :|| :|| :|| :||
          59 DEEKESQNIPAELISVYNSTVELNEEQAAPPEQPKEDPVEEEYYAKEVHKFTIKLMEKNP 118
Db
         119 OIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLK--VEQHVELYQKYSN 176
Qу
                        | \cdot | \cdot | \cdot | \cdot |
Db
         119 ---DKF------LWFNITDISQTLGLNRIISQVELRLLITTFPDGSEQRLELYQVIGN 167
         177 DSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEI 236
Qу
             Db
         168 KS-RYLESRFI--PNQRKWLSFDVTQTLKDWLQRSEAEQGFQLKMADNCDPQ-KTFQLKI 223
Qу
         237 NGFNSGRRGDLATIH-GMNRPFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFS 295
                   Db
         224 PGLVL-VRGDTETLAVNMPRPHILVMSLPLDGN---NSSKSRRKROTETDOV-----CTD 274
         296 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 355
Qу
             Db
         275 KSD-GCCVRSLYIDFRKDLGWKWIHEPSGYYANYCTGSCSFVWTSENKYSQVLALYKHHN 333
         356 PGASAAPCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKC 397
Qу
             Db
         334 PGASAQPCRVPQVLNPLPIFYYVGRQHKVEQLSNMIVKTCKC 375
RESULT 10
09ERB7
ID
    Q9ERB7
               PRELIMINARY;
                               PRT;
                                     399 AA.
AC
    O9ERB7;
DT
    01-MAR-2001 (TrEMBLrel. 16, Created)
DT
    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
    01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DT
DE
    Transforming growth factor-beta 2 (Fragment).
OS
    Mesocricetus auratus (Golden hamster).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC
    Mesocricetus.
OX
    NCBI TaxID=10036;
RN
    [1]
RP
    SEQUENCE FROM N.A.
    Ramesh G., Kondaiah P., Seshagiri P.B.;
RA
RT
    "Differential expression and selective localization of transforming
RT
    growth factor-beta isoforms in the hamster uterus during estrous
RT
    cycle.";
RL
    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AY007214; AAG02247.1; -.
DR
    HSSP; P08112; 2TGI.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
    Pfam; PF00019; TGF-beta; 1.
```

```
Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
FT
    NON_TER 1 1
FT
    NON TER
             399 399
    SEQUENCE 399 AA; 46078 MW; A6FF8E65EAFD5148 CRC64;
SQ
 Query Match
                    36.3%; Score 767.5; DB 11; Length 399;
 Best Local Similarity 43.1%; Pred. No. 5.9e-60;
 Matches 177; Conservative 60; Mismatches 121; Indels 53; Gaps 15;
         18 LLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-PGPLPEA 76
Qу
           Db
          4 LLHLVP--VALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEPDEVPPE 59
         77 VLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYDKFKGTP 128
Qу
           Db
         60 VISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHFPSENAIPPTFY-RP 118
        129 HSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----KYSNDSW 179
Qу
           Db
        119 YFRIVRFDVSMMEKNASN---LVKAEFRVFRLONPKARVAEORIELYOILKSKDLTSPTO 175
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSK 228
Qу
                      : :|
        176 RYIDSKVVKTRAEGEWLSFDVTDAVHEWLHHKDRNLGFKISLHCPCCTFVPFNNNIIPNK 235
Db
        229 DNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHSSRHRRD 279
Qу
                  Db
        236 SEELEARFAGIDGTSQHSSGHQETIKSTRKKNSGKTPHLLLMLLPSYRLESQOSNRRKK- 294
        280 YKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWS 339
Qу
                295 -----RALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWS 348
Db
        340 LDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNM 390
Qу
            Db
        349 SDTOHTKVLSLYNTINPEASASPCCVSHDLEPLTILYYIGNTPKIEOLSNM 399
RESULT 11
Q99K17
ID
    Q99K17
            PRELIMINARY; PRT; 362 AA.
AC
    O99K17;
DT
    01-JUN-2001 (TrEMBLrel. 17, Created)
    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Similar to transforming growth factor, beta 3 (Fragment).
GN
    TGFB3.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
```

```
RA
    Strausberg R.;
RL
    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; BC005513; AAH05513.1; -.
DR
    HSSP: P10600; 1TGJ.
DR
    MGD; MGI:98727; Tqfb3.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA 1; 1.
DR
FT
    NON TER
               1
SO
    SEQUENCE
             362 AA; 41486 MW; 0808E46180FDAE70 CRC64;
                     34.4%; Score 727; DB 11; Length 362;
 Query Match
 Best Local Similarity 44.0%; Pred. No. 2.1e-56;
 Matches 164; Conservative 52; Mismatches 113; Indels 44; Gaps
         58 RLASPPSQGDVPPGPLPEAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVL 112
Qу
           2 RVGSPPEPSVMT--HVPYQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFD 59
Db
        113 MVE---SGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVE 165
Qу
            Db
         60 MIQGLAEHNELAVCPKGITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTE 115
        166 QHVELYQKYSND----SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSA 221
Qу
            116 QRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISI 175
Db
        222 H-----SSSDSKDN---TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPL 265
Qу
                   176 HCPCHTFOPNGDILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKOKDHHNPHLILMMIPP 235
Db
        266 ERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGY 325
Qу
                            :
        236 HRLDSPGQGSQRK------KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGY 289
Db
        326 HANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVE 385
Qу
            Db
        290 YANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVE 349
        386 QLSNMIVRSCKCS 398
Qу
            Db
        350 QLSNMVVKSCKCS 362
RESULT 12
008714
ID
              PRELIMINARY; PRT; 130 AA.
    Q08714
    Q08714; O70331;
AC
```

```
DT
     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE
     Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN
OS
     Mesocricetus auratus (Golden hamster).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC.
     Mesocricetus.
OX
     NCBI TaxID=10036;
RN
RP
     SEQUENCE FROM N.A.
RC
     STRAIN=LVG (SYR);
     MEDLINE=93304479; PubMed=8317544;
RX
RA
     Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
RA
     Elovic A., McBride J., Gallagher G., Todd R.;
RT
     "Sequential expression of transforming growth factors alpha and beta 1
     by eosinophils during cutaneous wound healing in the hamster.";
RT
     Am. J. Pathol. 143:130-142(1993).
RL
RN
     SEQUENCE OF 26-115 FROM N.A.
RP
     STRAIN=SYRIAN; TISSUE=SPLEEN;
RC
RX
     MEDLINE=98234044; PubMed=9573100;
     Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RA
RT
     "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
     analysis of cytokine mRNA expression in experimental visceral
RT
RT
     leishmaniasis.";
RL
     Infect. Immun. 66:2135-2142(1998).
CC
     -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
         PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
         TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC
CC
         THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC
         REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC
         DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC
CC
     -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR
     EMBL; X60296; CAA42838.1; -.
DR
     EMBL; AF046214; AAC40099.1; -.
DR
     HSSP; P01137; 1KLA.
DR
     InterPro; IPR001839; TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
     ProDom; PD000357; TGFb; 1.
DR
DR
     SMART; SM00204; TGFB; 1.
DR
     PROSITE; PS00250; TGF BETA 1; 1.
KW
     Growth factor; Mitogen; Glycoprotein.
FT
     NON TER
                  1
                         1
     PROPEP
FT
                  <1
                         18
FT
                        130
                                  TRANSFORMING GROWTH FACTOR BETA 1.
     CHAIN
                  19
FT
                  25
                        34
     DISULFID
                                  BY SIMILARITY.
FT
     DISULFID
                  33
                         96
                                  BY SIMILARITY.
                       129
FT
     DISULFID
                  66
                                  BY SIMILARITY.
                        95
FT
     DISULFID
                  95
                                  INTERCHAIN (BY SIMILARITY).
                        93
FT
     CONFLICT
                  93
                                  G \rightarrow S (IN REF. 2).
     SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CCA77 CRC64;
SQ
                          32.9%; Score 696; DB 11; Length 130;
  Query Match
  Best Local Similarity 92.0%; Pred. No. 2.8e-54;
```

```
Matches 127; Conservative 0; Mismatches 3; Indels 8; Gaps
Qу
         261 MATPLERAOHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIH 320
             Db
           1 MATPLERAQHLQSSRHRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIH 52
         321 EPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGR 380
Qу
             Db
          53 EPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASAGPCCVPOALEPLPIVYYVGR 112
         381 KPKVEQLSNMIVRSCKCS 398
Qу
             113 KPKVEQLSNMIVRSYKCS 130
Db
RESULT 13
098854
ID
    Q98854
                PRELIMINARY;
                                 PRT;
                                        361 AA.
AC
    Q98854;
\mathsf{D}\mathbf{T}
    01-FEB-1997 (TrEMBLrel. 02, Created)
DT
    01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DΕ
    Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
GN
    TGFB2.
OS
    Cyprinus carpio (Common carp).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC
    Cyprinidae; Cyprinus.
OX
    NCBI TaxID=7962;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=HEART;
RX
    MEDLINE=97354301; PubMed=9210595;
    Sumathy K., Desai K.V., Kondaiah P.;
RA
RT
    "Isolation of transforming growth factor-beta2 cDNA from a fish,
RT
    Cyprinus carpio by RT-PCR.";
RL
    Gene 191:103-107(1997).
CC
    -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC
        DEPENDENT T-CELL GROWTH.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; U66874; AAB62983.1; -.
    HSSP; P08112; 2TGI.
DR
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    InterPro; IPR003911; TGF_TGFb.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
KW
    Growth factor; Mitogen; Glycoprotein.
    NON TER
FT
                1
                        1
FT
    PROPEP
                <1
                      257
                258
                                TRANSFORMING GROWTH FACTOR BETA 2.
FT
    CHAIN
                      361
FT
    DISULFID
               264
                      273
                               BY SIMILARITY.
```

```
272
    DISULFID
              334 334
FT
                            INTERCHAIN (BY SIMILARITY).
                    30
FT
    CARBOHYD
              30
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
              98
                    98
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
             199
                    199
                            N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    NON TER
             361
                    361
    SEQUENCE 361 AA; 41931 MW; 94D930FA970A3FD3 CRC64;
SO
 Query Match
                      32.2%; Score 681; DB 13; Length 361;
 Best Local Similarity 41.3%; Pred. No. 2.7e-52;
 Matches 155; Conservative 55; Mismatches 115; Indels 50; Gaps
Qу
         52 QILSKLRLASPPSQGDVPPGP--LPEAVLALYNSTRDRVAGESVEPEPEPE----ADYY 104
            Db
          1 QILCKLKLSCPP---EIYPEPEEVSRDIIAIYNSTRDLLQEKANERAATCERQRTGEEYY 57
        105 AKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL- 160
Qу
            58 AKEVHKIDMQPFYPAENVIPTKHY-NPYFRRLRFDVSSMEKNASN---LVKAELRIFRLO 113
Db
        161 --KLKV-EQHVELYQ-----KYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRRE 212
QУ
             Db
        114 NPKARVSEQRIELYQILGHKDLTSPTQRYIDSKVVRTRTEGEWLSFDVTEAVSEWLLHRD 173
        213 AIEGFRLSAHSSS------DSKDNTLHVEINGFNSG--RRGDLATI----HGMNR 255
Qу
                                :| | : | ||
              |\cdot|::|\cdot|
        174 RNNGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDDSFVHGGDLKMFKKRRHSGQS 233
Db
        256 PFLLLMATPLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 315
Qу
            234 PHLLLMLLPSYRLESQHKS-HRQ-----KRALDAAFCFRNVQDNCCLRSLYIDFKKDLG 286
Db
        316 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 375
Qу
            287 WKWIHEPKGYNANFCAGACPYLWSADTOHSNILGLYNTINPEASASPCCVSODLEPLTIL 346
Db
        376 YYVGRKPKVEOLSNM 390
QУ
           Db
        347 YYIGKTPKIEOLSNM 361
RESULT 14
095N80
ID
    O95N80
              PRELIMINARY; PRT; 124 AA.
AC
    Q95N80;
DT
    01-DEC-2001 (TrEMBLrel. 19, Created)
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
    Transforming growth factor beta 1 (Fragment).
DΕ
OS
    Canis familiaris (Dog).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC
    NCBI TaxID=9615;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RP
    Fonfara S., Groene A., Baumgaertner W.;
RA
RT
    "Sequence of canine transforming growth factor beta 1 mRNA in DH82-
```

BY SIMILARITY.

FT

DISULFID

335

```
RT
     cells.";
RL
     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC
     -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
     EMBL; AF349538; AAK54072.1; -.
DR
     InterPro; IPR001839; TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     ProDom; PD000357; TGFb; 1.
     SMART; SM00204; TGFB; 1.
DR
DR
     PROSITE; PS00250; TGF BETA 1; 1.
FT
    NON TER
                1
FT
    NON TER
                124
                      124
SO
    SEQUENCE
               124 AA; 14329 MW; 21D185218E5556DB CRC64;
  Query Match
                        32.1%; Score 679; DB 6; Length 124;
  Best Local Similarity 93.2%; Pred. No. 8.5e-53;
 Matches 123; Conservative 0; Mismatches
                                               1; Indels
                                                             8; Gaps
                                                                         1;
         264 PLERAQHLHSSRHRRDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPK 323
Qу
             Db
           1 PLERAQHLHSSRQRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPK 52
Qу
         324 GYHANFCLGPCPYIWSLDTQYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPK 383
             Db
          53 GYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPK 112
Qу
         384 VEQLSNMIVRSC 395
             Db
         113 VEQLSNMIVRSC 124
RESULT 15
002730
ΙD
    002730
                PRELIMINARY;
                                 PRT:
                                        112 AA.
AC
    002730; 097501;
DT
     01-JUL-1997 (TrEMBLrel. 04, Created)
     01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
DE
    Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN
    TGFB1 OR TGF-BETA-1.
OS
    Oryctolagus cuniculus (Rabbit).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX
    NCBI TaxID=9986;
RN
     [1]
RP
    SEQUENCE FROM N.A.
RA
    Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL
    Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN
    SEQUENCE OF 2-99 FROM N.A.
RP
RA
    Inoue K., Kawabe Y., Kodama T.;
RL
    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC
        THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC
        REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC
        DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
```

```
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF000133; AAB53806.1; -.
DR
    EMBL; AB020217; BAA36950.1; -.
DR
    HSSP; P01137; 1KLA.
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR001839; TGFb.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein.
FT
    NON TER
                1
                      1
FT
    CHAIN
                 1
                     112
                              TRANSFORMING GROWTH FACTOR BETA 1.
                    16
FT
    DISULFID
                7
                              BY SIMILARITY.
    DISULFID
                             BY SIMILARITY.
FT
                15
                     78
FT
    DISULFID
               44
                    109
                             BY SIMILARITY.
FT
    DISULFID
               48 111
                             BY SIMILARITY.
                     77
FT
    DISULFID
               77
                              INTERCHAIN (BY SIMILARITY).
FT
    CONFLICT
               2
                      3
                              LD \rightarrow FS (IN REF. 2).
                     92
FT
    CONFLICT
               85
                             PLPIVYYV -> ATAHRVTTL (IN REF. 2).
SO
    SEQUENCE 112 AA; 12795 MW; 53C5B7D46355A6F3 CRC64;
 Query Match
                       30.2%; Score 638; DB 6; Length 112;
 Best Local Similarity 100.0%; Pred. No. 3.3e-49;
                                            0; Indels
 Matches 112; Conservative 0; Mismatches
                                                         0; Gaps
                                                                     0;
Qу
         287 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 346
            Db
          1 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60
Qу
         347 VLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 398
            Db
         61 VLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 112
```

Search completed: October 28, 2003, 09:12:23

Job time : 33.909 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 1415.77 Seconds

(without alignments)

10489.161 Million cell updates/sec

Title: US-10-017-372E-10

Perfect score: 363

Sequence: 1 gactacaaggatgacgacga.....gttcctgcaagtgcagctga 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2888711 segs, 20454813386 residues Searched:

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl: *

1: gb ba:*

2: gb htg:*

3: gb in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb pl:*

9: gb pr:* 10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em ba:*

16: em fun:*

17: em hum:*

18: em_in:*

19: em mu:*

20: em_om:*

21: em_or:*

22: em_ov:* 23: em_pat:*

24: em ph:*

25: em pl:*

26: em ro:*

27: em sts:*

```
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

કૃ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	פת	ID	Description
NO.	30016	Maccii	nengun			Description
1	339	93.4	1326	6	AX338213	AX338213 Sequence
2	339	93.4	1605	4	SSTGFBR	Y00111 Porcine mRN
3	339	93.4	1750	4	GGTGFB1	X12373 Porcine mRN
4	339	93.4	2221	4	AF461808	AF461808 Sus scrof
5	339	93.4	3206	4	PIGTGFB1A	M23703 Sus scrofa
6	312.8	86.2	489	6	AX455100	AX455100 Sequence
7	312.8	86.2	1369	4	DOGTGFB1A	L34956 Canine tran
8	312.2	86.0	1173	4	OATGFB1	X76916 O.aries mRN
9	311.8	85.9	1561	9	AGMTGFB	M16658 Simian tran
10	310.2	85.5	339	6	AR036686	AR036686 Sequence
11	310.2	85.5	1560	6	108268	108268 Sequence 2
12	309.2	85.2	1560	6	106216	I06216 Sequence 2
13	309	85.1	1117	4	BOVTGFB	M36271 Bovine tran
14	308.6	85.0	339	4	OCAF000133	AF000133 Oryctolag
15	308.6	85.0	339	6	A18277	A18277 H.sapiens T
16	308.6	85.0	339	6	A23751	A23751 TGF-beta1 c
17	308.6	85.0	339	6	A48549	A48549 Sequence 1
18	308.6	85.0	339	6	A48563	A48563 Sequence 1
19	308.6	85.0	339	6	I56854	I56854 Sequence 1
20	308.6	85.0	650	6	AX336646	AX336646 Sequence
21	308.6	85.0	650	9	HUMTGFBA	M38449 Homo sapien
22	308.6	85.0	699	6	I05434	I05434 Sequence 4
23	308.6	85.0	862	6	I03312	I03312 Sequence 3
24	308.6	85.0	1176	6	AX481432	AX481432 Sequence
25	308.6	85.0	1176	6	AX615127	AX615127 Sequence
26	308.6	85.0	1176	6	AX615128	AX615128 Sequence
27	308.6	85.0	1746	9	BC022242	BC022242 Homo sapi
28	308.6	85.0	1780	9	BC000125	BC000125 Homo sapi
29	308.6	85.0	1780	9	BC001180	BC001180 Homo sapi
30	308.6	85.0	1821	6	E03028	E03028 DNA encodin
31	308.6	85.0	2537	6	A06669	A06669 Synthetic m
32	308.6	85.0	2745	9	HSTGFB1	X02812 Human mRNA
33	308.2	84.9	337	6	AR198575	AR198575 Sequence

```
34
           307
                84.6
                       1266 6 AX455875
                                                          AX455875 Sequence
    35
           307
                84.6
                       2527 6 E00973
                                                          E00973 cDNA encodi
                                                          BT007245 Homo sapi
    36
         306.6
                84.5
                       1173 9 BT007245
    37
                                                           BT007866 Synthetic
        306.6
                84.5
                       1173 12 BT007866
    38
                       1569 6 106221
           306
                84.3
                                                          I06221 Sequence 3
                        469 10 MATGFB1
    39
         303.8
                83.7
                                                           X60296 M.auratus m
    40
         303.6
                83.6
                        334 4 SHPGFB1W
                                                          L36038 Ovis aries
    41
        302.8
                83.4
                        374
                             4 AF349538
                                                          AF349538 Canis fam
    42
        302.2
                83.3 1173 4 ECRGFB1
                                                          X99438 E.caballus
        300.6
    43
               82.8
                       1187 4 AF175709
                                                         AF175709 Equus cab
        300.6 82.8
                       1597 10 AF191297
    44
                                                           AF191297 Cavia por
    45
        287.8 79.3
                       1579 10 MUSTGFRNA
                                                           M13177 Mouse trans
                                   ALIGNMENTS
RESULT 1
AX338213
LOCUS
           AX338213
                                   1326 bp
                                              DNA
                                                      linear
                                                               PAT 09-JAN-2002
DEFINITION Sequence 1 from Patent W00181404.
ACCESSION
           AX338213
           AX338213.1 GI:18128750
VERSION
KEYWORDS
            Sus scrofa (pig)
SOURCE
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  AUTHORS
            Strober, W., Nakamura, K., Kitani, A. and Fuss, I.J.
  TITLE
            Inducible plasmid vector encoding tgf-_g(b) and uses thereof
  JOURNAL
            Patent: WO 0181404-A 1 01-NOV-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
                    Location/Qualifiers
     source
                     1. .1326
                     /organism="Sus scrofa"
                     /mol type="genomic DNA"
                     /db xref="taxon:9823"
     CDS
                     16. .1188
                     /note="unnamed protein product"
                     /codon start=1
                     /protein id="CAD20538.1"
                    /db xref="GI:18128751"
                     /translation="MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                    RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                    YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                    KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                    LSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
                    RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                    QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT
               263 a
                        438 c
                                 392 g
                                          233 t
ORIGIN
  Query Match
                         93.4%; Score 339; DB 6; Length 1326;
  Best Local Similarity 100.0%; Pred. No. 1.4e-60;
```

0; Indels

0; Gaps

0;

Matches 339; Conservative 0; Mismatches

```
Qу
        Db
       Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
          Db
       910 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 969
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          970 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1029
Db
       Qу
           1030 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCGTGCCG 1089
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
      1090 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1149
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
QУ
           Db
      1150 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1188
RESULT 2
SSTGFBR
LOCUS
         SSTGFBR
                           1605 bp
                                   mRNA
                                          linear
                                                MAM 27-MAR-1995
DEFINITION Porcine mRNA for transforming growth factor-beta (TFG) precursor.
ACCESSION
         Y00111
         Y00111.1 GI:2129
VERSION
KEYWORDS
         transforming growth factor-beta.
         Sus scrofa (pig)
SOURCE
 ORGANISM Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
           (bases 1 to 1605)
 AUTHORS
         Derynck, R. and Rhee, L.
 TITLE
         Sequence of the porcine transforming growth factor-beta precursor
         Nucleic Acids Res. 15 (7), 3187 (1987)
 JOURNAL
 MEDLINE
         87174844
  PUBMED
         3470708
FEATURES
                Location/Qualifiers
   source
                1. .1605
                /organism="Sus scrofa"
                /mol type="mRNA"
                /db xref="taxon:9823"
                /tissue_type="ovary"
                /clone lib="lambda qt10"
   CDS
                404. .1576
                /note="TFG-beta precursor (AA 1-390)"
                /codon_start=1
                /protein id="CAA68291.1"
                /db xref="GI:2130"
                /db xref="SWISS-PROT:P07200"
                /translation="MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
```

```
KLKVEOHVELYOKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFR
                LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
                RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
   mat peptide
                1238. . 1573
                /product="mature TFG-beta"
                647. .655
   misc feature
                /note="pot. N-glycosylation site"
   misc feature
                809. .817
                /note="pot. N-glycosylation site"
BASE COUNT
            298 a
                   572 c
                         437 g
                                 298 t
ORIGIN
 Query Match
                    93.4%; Score 339; DB 4; Length 1605;
 Best Local Similarity
                   100.0%; Pred. No. 1.4e-60;
 Matches 339; Conservative
                         0: Mismatches
                                       0; Indels
                                                     Gaps
                                                  0;
                                                           0;
        Qу
           Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           Db
       1298 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1357
Qу
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
           Db
       1358 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1417
Qу
       Db
       1418 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 1477
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           1478 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1537
Db
Oy
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
       1538 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1576
RESULT 3
GGTGFB1
LOCUS
         GGTGFB1
                           1750 bp
                                    mRNA
                                          linear
                                                MAM 27-MAR-1996
DEFINITION Porcine mRNA for transforming growth factor-beta 1.
ACCESSION
         X12373
VERSION
         X12373.1 GI:63808
KEYWORDS
         transforming growth factor-beta 1.
SOURCE
         Sus scrofa (pig)
 ORGANISM Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
           (bases 1 to 1750)
 AUTHORS
         Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
```

Nucleotide sequence of chicken transforming growth factor-beta 1

TITLE

YYAKEVTRVLMLESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL

```
(TGF-beta 1)
 JOURNAL
          Nucleic Acids Res. 16 (17), 8730 (1988)
 MEDLINE
          88335639
  PUBMED
          3166520
REFERENCE
             (bases 1 to 1750)
 AUTHORS
          Jakowlew, S.B.
 TITLE
          Direct Submission
 JOURNAL
          Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
          health, National Cancer Institute, Laboratory of Chemoprevention,
          Building 41, Room B902, Bethesda, Maryland 20892, USA
COMMENT
          The submitters believe that the chicken cDNA library was
          contaminated with porcine cDNA, and that the sequence is infact
          porcine TGF-beta-1.
                              27-MAR-1996.
FEATURES
                  Location/Qualifiers
                  1. .1750
    source
                  /organism="Sus scrofa"
                  /mol type="mRNA"
                  /strain="white leghorn"
                  /db xref="taxon:9823"
                  /clone="pTGFB-ChX119"
                  /cell type="chondrocyte"
                  1. .1750
    gene
                  /gene="TGF-beta 1"
    5'UTR
                  1. .446
                  /gene="TGF-beta 1"
    CDS
                  447. .1622
                  /gene="TGF-beta 1"
                  /codon start=1
                  /product="transforming growth factor"
                  /protein_id="CAA30933.1"
                  /db xref="GI:63809"
                  /db xref="SWISS-PROT:P07200"
                  translation="MPPSGPGLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK/
                  RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                  YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                  KLKVEQHVELYQKYSNDSWGYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                  LSAHCSCDSKDNTLHVEINAGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSR
                  HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD
                  TQYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS"
    mat peptide
                  1285. .1619
                  /gene="TGF-beta 1"
    3'UTR
                  1620. .1750
                  /gene="TGF-beta 1"
BASE COUNT
              325 a
                      627 c
                              479 q
                                      319 t
ORIGIN
 Query Match
                       93.4%; Score 339; DB 4; Length 1750;
 Best Local Similarity
                       100.0%; Pred. No. 1.3e-60;
 Matches 339; Conservative
                            0; Mismatches
                                             0; Indels
                                                             Gaps
                                                                    0;
Qу
         Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
            1344 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1403
Db
```

```
145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
             1404 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1463
Db
         205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCGTGCCG 264
Qу
             Db
        1464 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCG 1523
         265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
             Db
        1524 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1583
         325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
             Db
        1584 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1622
RESULT 4
AF461808
LOCUS
          AF461808
                                2221 bp
                                          mRNA
                                                 linear MAM 03-JAN-2002
DEFINITION Sus scrofa transforming growth factor beta 1 (TGFB1) mRNA, complete
ACCESSION
          AF461808
          AF461808.1 GI:18042250
VERSION
KEYWORDS
SOURCE
          Sus scrofa (pig)
  ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
             (bases 1 to 2221)
 AUTHORS
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
          Polymorphism in the porcine transforming growth factor beta 1 gene
 TITLE
 JOURNAL
          Unpublished
REFERENCE
             (bases 1 to 2221)
 AUTHORS
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
          Direct Submission
 TITLE
 JOURNAL
          Submitted (20-DEC-2001) Institute of Animal Breeding Science,
          University of Bonn, Endenicher Allee 15, Bonn 53115, Germany
FEATURES
                   Location/Qualifiers
                   1. .2221
    source
                   /organism="Sus scrofa"
                   /mol type="mRNA"
                   /db xref="taxon:9823"
                   /chromosome="6"
                   1. .2221
    gene
                   /gene≈"TGFB1"
    CDS
                   1. .1173
                   /gene="TGFB1"
                   /note="cytokine"
                   /codon start=1
                   /product="transforming growth factor beta 1"
                   /protein id="AAL57902.1"
                   /db xref="GI:18042251"
                   /translation="MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
                   RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
                   YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
```

KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"

3'UTR 1174. .2221 /gene="TGFB1"

BASE COUNT 504 a 616 c 649 g 452 t

ORIGIN

```
Query Match
                93.4%;
                     Score 339; DB 4; Length 2221;
 Best Local Similarity
                100.0%; Pred. No. 1.3e-60;
 Matches 339; Conservative
                     0; Mismatches
                                0; Indels
                                         0; Gaps
                                                 0;
Qу
       Db
      Qу
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
         Db
      895 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 954
      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
         Db
      955 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1014
      205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 264
QУ
         1015 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCG 1074
Db
      265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
         Db
     1075 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1134
      325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
QУ
         Db
     1135 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1173
```

RESULT 5 PIGTGFB1A

TITLE

LOCUS PIGTGFB1A 3206 bp mRNA linear MAM 31-MAR-1995 DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.

ACCESSION M23703

VERSION M23703.1 GI:755044

KEYWORDS transforming growth factor-beta-1.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 3206)

AUTHORS Kondaiah, P., Van Obberghen-Schilling, E., Ludwig, R.L., Dhar, R., Sporn, M.B. and Roberts, A.B.

cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.

Evidence for alternate splicing and polyadenylation JOURNAL J. Biol. Chem. 263 (34), 18313-18317 (1988)

MEDLINE 89054010 PUBMED 2461367

```
On Apr 1, 1995 this sequence version replaced gi:341017.
         Original source text: Sus scrofa (strain miniature swine) cDNA to
         mRNA.
FEATURES
               Location/Qualifiers
               1. .3206
   source
               /organism="Sus scrofa"
               /mol_type="mRNA"
               /strain="miniature swine"
               /db xref="taxon:9823"
               /cell type="peripheral blood lymphocyte"
               1. .3206
   gene
               /gene="TGF-beta-1"
   CDS
               906. .2078
               /gene="TGF-beta-1"
               /codon start=1
               /product="transforming growth factor-beta-1"
               /protein id="AAA64616.1"
               /db xref="GI:755045"
               translation="MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK/
               RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
               YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
               KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
               LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
               RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
               OYSKVLALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS"
               3186. .3191
   polyA signal
               /gene="TGF-beta-1"
   polyA site
               3206
               /gene="TGF-beta-1"
BASE COUNT
                 1041 c
            645 a
                         924 g
                                596 t
ORIGIN
 Query Match
                   93.4%; Score 339; DB 4; Length 3206;
                   100.0%; Pred. No. 1.3e-60;
 Best Local Similarity
 Matches 339; Conservative 0; Mismatches 0; Indels
                                                0; Gaps
        Qу
          Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
          1800 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1859
Db
       145 GCCAATTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
      1860 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1919
       Qу
          Db
      265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          1980 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 2039
Db
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
```

COMMENT

```
RESULT 6
AX455100
LOCUS
         AX455100
                            489 bp
                                    DNA
                                          linear
                                                 PAT 06-JUL-2002
         Sequence 167 from Patent W00208453.
DEFINITION
ACCESSION
         AX455100
         AX455100.1 GI:21714285
VERSION
KEYWORDS
         Canis familiaris (dog)
SOURCE
         Canis familiaris
 ORGANISM
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
 AUTHORS
         Farr, S.B., Pickett, G.G., Neft, R.E. and Dunn, R.T.
 TITLE
         Canine toxicity genes
 JOURNAL
         Patent: WO 0208453-A 167 31-JAN-2002;
         Phase-1 Molecular Toxicology (US)
FEATURES
                Location/Qualifiers
                1. .489
    source
                /organism="Canis familiaris"
                /mol type="genomic DNA"
                /db xref="taxon:9615"
                                  76 t
BASE COUNT
             84 a
                   183 c
                          145 g
                                         1 others
ORIGIN
                    86.2%; Score 312.8; DB 6; Length 489;
 Query Match
 Best Local Similarity
                    95.0%; Pred. No. 4.3e-55;
 Matches 323; Conservative
                         0; Mismatches
                                     17; Indels
                                                  0; Gaps
                                                            0;
        Qy
           71 GGCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCT 130
Db
        84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
Qу
           131 CTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCA 190
Db
       144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
Qу
            191 CGCTAACTTCTGCCTGGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAA 250
Db
       Qy
           251 GGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCGCGTCGGCGGCGCGCGTGCTGCGTGCC 310
Db
       264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
Qу
           311 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 370
Db
       324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           371 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 410
Db
```

```
RESULT 7
DOGTGFB1A
LOCUS
            DOGTGFB1A
                                    1369 bp
                                               mRNA
                                                       linear
                                                                MAM 30-OCT-1994
DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete
ACCESSION
            L34956
            L34956.1 GI:516071
VERSION
KEYWORDS
            homologue; transforming growth factor-beta 1.
SOURCE
            Canis familiaris (dog)
 ORGANISM Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
               (bases 1 to 1369)
 AUTHORS
            Manning, A.M., Auchampach, J.A., Drong, R.F. and Slightom, J.L.
  TITLE
            Cloning of a canine cDNA homologous to human transforming growth
            factor-beta 1 (TGFbeta1)
  JOURNAL
            Unpublished (1994)
COMMENT
            Original source text: Canis familiaris adult jugular vein
            endothelial cDNA to mRNA.
FEATURES
                     Location/Oualifiers
                     1. .1369
    source
                     /organism="Canis familiaris"
                     /mol type="mRNA"
                     /db xref="taxon:9615"
                     /cell type="LPS-activated"
                     /tissue type="jugular vein endothelial"
                     /dev stage="adult"
                     1. .1369
    gene
                     /gene="TGFB1"
     5'UTR
                     1. .57
                     /gene="TGFB1"
     CDS
                     58. .1230
                     /gene="TGFB1"
                     /function="anti-inflammatory agent"
                     /note="precursor"
                     /codon_start=1
                     /product="transforming growth factor-beta 1"
                     /protein id="AAA51458.1"
                     /db xref="GI:516072"
                     /translation="MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRK
                     RIEAIRGOILSKLRLSSPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                     YYAKEVTRVLMVENTNKI YEKVKKSPHSI YMLFNTSELREAVPEPVLLSRAELRLLRL
                     KLKAEQHVELYQKYSNDSWRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFR
                     LSAHCSCDSKDNTLQVDINGFSSSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRO
                     RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                     QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
     mat peptide
                     1039. .1227
                     /gene="TGFB1"
                     /product="transforming growth factor-beta 1"
     3'UTR
                     1231. .1369
                     /gene="TGFB1"
BASE COUNT
                264 a
                                  415 g
                                           216 t
                                                      1 others
                         473 c
ORIGIN
  Query Match
                          86.2%; Score 312.8; DB 4; Length 1369;
 Best Local Similarity 95.0%; Pred. No. 3.9e-55;
                                                17; Indels
 Matches 323; Conservative 0; Mismatches
                                                                 0; Gaps
                                                                              0;
```

```
Qу
        Db
        891 GGCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCT 950
        84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
Qу
           Db
        951 CTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCA 1010
        144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
Qу
            Db
       1011 CGCTAACTTCTGCCTGGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAA 1070
        204 GGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCGTGCC 263
Qу
           Db
       Qу
        264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
           Db
       1131 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 1190
        324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
QУ
           Db
       1191 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1230
RESULT 8
OATGFB1
LOCUS
         OATGFB1
                            1173 bp
                                     mRNA
                                           linear
                                                  MAM 18-APR-1995
DEFINITION O.aries mRNA for transforming growth factor-beta I.
ACCESSION
         X76916
VERSION
         X76916.1 GI:496648
KEYWORDS
         TGF-beta 1; transforming growth factor-beta 1.
SOURCE
         Ovis aries (sheep)
 ORGANISM Ovis aries
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
         Bovidae; Caprinae; Ovis.
REFERENCE
 AUTHORS
         Woodall, C.J., McLaren, L.J. and Watt, N.J.
 TITLE
         Sequence and chromosomal localisation of the gene encoding ovine
         latent transforming growth factor-beta 1
 JOURNAL
         Gene 150 (2), 371-373 (1994)
 MEDLINE
         95121932
  PUBMED
         7821809
         2 (bases 1 to 1173)
REFERENCE
 AUTHORS
         Woodall, C.
 TITLE
         Direct Submission
 JOURNAL
         Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of
         Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
         Edinburgh EH9 IQH, UK
FEATURES
                Location/Qualifiers
                1. .1173
    source
                /organism="Ovis aries"
                /mol type="mRNA"
                /db xref="taxon:9940"
    CDS
                1. .1173
```

```
/codon start=1
                  /product="transforming growth factor-beta 1"
                  /protein id="CAA54242.1"
                  /db xref="GI:496649"
                  /db xref="SWISS-PROT:P50414"
                  /translation="MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRK
                  GIEAIRGQILSKLRLASPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEAD
                  YYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRL
                  KLKVEOHVELYOKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVROWLTHREEIEGFR
                  LSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
                  RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                  QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
    mat peptide
                  835. .1170
                  /product="transforming growth factor-beta 1"
BASE COUNT
              245 a
                     378 c
                             336 g
                                     214 t.
ORIGIN
 Query Match
                      86.0%; Score 312.2; DB 4; Length 1173;
 Best Local Similarity
                      93.4%; Pred. No. 5.3e-55;
 Matches 326; Conservative
                            0; Mismatches
                                          23: Indels
                                                        0; Gaps
                                                                   0;
         15 CGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 74
QУ
                    Db
        825 CCACCGCCGAGCCCTGGACACCAACTACTGCTTCAGCTCCACAGAAAAGAACTGCTGTGT 884
         75 GCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAA 134
Qу
             885 TCGTCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCACGAACCCAA 944
Dh
        135 GGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCA 194
QУ
            Db
        945 GGGCTACCACGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTGGACACACA 1004
        195 GTACAGCAAGGTCCTGGCTCTGTACAACCAGCACACCCGGGCGCGCTCGGCGGCGCCGTG 254
Qу
            1005 GTACAGCAAGGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCATCGGCGGCGCCGTG 1064
Db
        255 CTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAA 314
Qу
            Db
       1065 CTGCGTGCCTCAGGCGCTGGAACCCCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAA 1124
        315 GGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
            Db
       1125 GGTGGAGCAGTTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1173
RESULT 9
AGMTGFB
LOCUS
                                                       PRI 27-APR-1993
          AGMTGFB
                               1561 bp
                                                linear
                                        mRNA
DEFINITION Simian transforming growth factor-beta (TGF) mRNA, complete cds.
ACCESSION
          M16658
VERSION
          M16658.1 GI:176552
KEYWORDS
          growth factor; transforming growth factor-beta.
SOURCE
          Cercopithecus aethiops (African green monkey)
 ORGANISM
          Cercopithecus aethiops
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
```

```
Cercopithecinae; Cercopithecus.
REFERENCE
            (bases 1 to 1561)
 AUTHORS
         Sharples, K., Plowman, G.D., Rose, T.M., Twardzik, D.R. and
         Purchio, A.F.
         Cloning and sequence analysis of simian transforming growth
 TITLE
         factor-beta cDNA
 JOURNAL
         DNA 6 (3), 239-244 (1987)
         87246074
 MEDLINE
  PUBMED
         3474130
COMMENT
         Original source text: African green monkey cells (cell line
         BSC-40), cDNA to mRNA, clone pTGF-beta-2.
FEATURES
                Location/Qualifiers
    source
                1. .1561
                /organism="Cercopithecus aethiops"
                /mol_type="mRNA"
                /db xref="taxon:9534"
    CDS
                262. .1434
                /note="transforming growth factor-beta precursor"
                /codon start=1
                /protein id="AAA35369.1"
                /db xref="GI:176553"
                translation="MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRK/
                RIETIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                YYAKEVTRVLMVETHNEIYDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                KLKVEOHVELYOKYSNNSWRYLSNRLLAPSNSPEWLSFDVTGVVROWLSRGGEIEGFR
                LSAHCSCDSKDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
                RRALDTNYCFSSTEKNCCVRQLYI DFRKDLGWKWI HEPKGYHANFCLGPCPYI WSLDT
                OYSKVLALYNOHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                262. .1095
    sig peptide
                /note="transforming growth factor-beta signal peptide"
    mat peptide
                1096. .1431
                /product="transforming growth factor-beta"
BASE COUNT
            301 a
                   547 c
                           446 g
                                  267 t
ORIGIN
 Query Match
                    85.9%; Score 311.8; DB 9; Length 1561;
                    95.0%; Pred. No. 6.2e-55;
 Best Local Similarity
        322; Conservative
                          0; Mismatches
                                       17;
                                           Indels
                                                    0; Gaps
                                                             0;
        Qу
           Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           1156 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1215
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           1216 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1275
Db
       Qу
           Db
       1276 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCGTGCCG 1335
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
```

```
1336 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1395
Db
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
          Db
      1396 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1434
RESULT 10
AR036686
LOCUS
        AR036686
                          339 bp
                                  DNA
                                       linear PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5800811.
ACCESSION
        AR036686
VERSION
        AR036686.1 GI:5954542
KEYWORDS
SOURCE
        Unknown.
 ORGANISM
        Unknown.
        Unclassified.
          (bases 1 to 339)
REFERENCE
 AUTHORS
        Hall, F.L., Nimni, M.E., Tuan, T.-L., Wu, L. and Cheung, D.T.
 TITLE
        Artificial skin prepared from coclagen matrix containing
        transforming growth factor-.beta. having a collagen binding site
 JOURNAL
        Patent: US 5800811-A 29 01-SEP-1998;
FEATURES
               Location/Qualifiers
               1. .339
   source
               /organism="unknown"
BASE COUNT
            66 a
                  113 c
                        100 q
                               60 t
ORIGIN
                  85.5%; Score 310.2; DB 6; Length 339;
 Query Match
 Best Local Similarity
                  94.7%; Pred. No. 1.5e-54;
 Matches 321; Conservative 0; Mismatches
                                   18: Indels
                                               0; Gaps
                                                        0:
       Qу
          Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
QУ
          Db
       121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
       Qу
          181 GTCCTGGCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCGCGCA40
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
       241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
```

301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339

Db

```
RESULT 11
I08268
LOCUS
         I08268
                                          linear PAT 02-DEC-1994
                            1560 bp
                                    DNA
DEFINITION Sequence 2 from Patent EP 0373994.
ACCESSION
         I08268
         I08268.1 GI:589017
VERSION
KEYWORDS
SOURCE
         Unknown.
 ORGANISM
        Unknown.
         Unclassified.
REFERENCE
           (bases 1 to 1560)
 AUTHORS
         Purchio, A.F., Gentry, L., Twardzik, D. and Brunner, A.M.
 TITLE
         Cloning and expression of simian transforming growth factor-beta 1
         Patent: EP 0373994-A1 2 20-JUN-1990;
 JOURNAL
FEATURES
                Location/Qualifiers
    source
                1. .1560
                /organism="unknown"
BASE COUNT
            301 a
                   542 c
                          444 g
                                 267 t
                                          6 others
ORIGIN
 Query Match
                    85.5%; Score 310.2; DB 6; Length 1560;
                    94.7%; Pred. No. 1.3e-54;
 Best Local Similarity
 Matches 321; Conservative
                         0; Mismatches
                                      18;
                                          Indels
                                                  0; Gaps
                                                            0:
        Qу
           Db
Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
       1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
Dh
       205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGGGGGCGCGTGCTGCGTGCCG 264
Qу
           1275 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCGTGCCG 1334
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
       1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       1395 CTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
RESULT 12
I06216
LOCUS
                                          linear PAT 02-DEC-1994
         I06216
                            1560 bp
                                    DNA
DEFINITION
         Sequence 2 from Patent EP 0293785.
ACCESSION
         I06216
VERSION
         I06216.1 GI:590649
KEYWORDS
```

SOURCE

Unknown.

```
ORGANISM Unknown.
         Unclassified.
REFERENCE
           (bases 1 to 1560)
 AUTHORS
         Purchio, A.F., Gentry, L. and Twardzik, D.
 TITLE
         Cloning and expression of simian transforming growth factor-SS1
 JOURNAL
         Patent: EP 0293785-A2 2 07-DEC-1988;
FEATURES
                Location/Qualifiers
   source
                1. .1560
                /organism="unknown"
BASE COUNT
            301 a
                   547 c
                         442 g
                                267 t 3 others
ORIGIN
 Query Match
                   85.2%; Score 309.2; DB 6; Length 1560;
 Best Local Similarity 94.4%; Pred. No. 2.2e-54;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                 0; Gaps
                                                          0;
        Qу
          1095 GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTNCGTGCGGCAGCTG 1154
Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
          1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
Dh
       Qу
          Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
Db
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
          Db
      1395 CTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
RESULT 13
BOVTGFB
LOCUS
         BOVTGFB
                           1117 bp
                                   mRNA
                                         linear
                                                MAM 27-APR-1993
DEFINITION Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3' end.
ACCESSION
         M36271
         M36271.1 GI:163747
VERSION
KEYWORDS
         transforming growth factor-beta 1.
SOURCE
         Bos taurus (cow)
 ORGANISM
        Bos taurus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
         Bovidae; Bovinae; Bos.
REFERENCE
         1 (bases 1 to 1117)
 AUTHORS
         Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B.
         and Baker, C.C.
```

Complementary deoxyribonucleic acid cloning of bovine transforming

TITLE

```
growth factor-beta 1
 JOURNAL
         Mol. Endocrinol. 1 (10), 693-698 (1987)
 MEDLINE
          91042552
  PUBMED
          3153459
COMMENT
          Original source text: Bovine fibropapilloma, cDNA to mRNA, (library
          of Okayama and Berg).
FEATURES
                 Location/Qualifiers
                 1. .1117
    source
                 /organism="Bos taurus"
                 /mol type="mRNA"
                 /db xref="taxon:9913"
    CDS
                 <1. .950
                 /note="transforming growth factor-beta-1 precursor"
                 /codon start=3
                 /protein id="AAA30778.1"
                 /db xref="GI:163748"
                 /translation="AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNK
                 I YDKMKSSSHSI YMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNN
                 SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVD
                 INGFSSGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRALDTNYCFSSTEKNC
                 CVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGAS
                 AAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS"
                 612. .947
    mat peptide
                 /product="transforming growth factor-beta-1"
BASE COUNT
             244 a
                    379 c
                            301 g
                                   193 t
ORIGIN
                     85.1%; Score 309; DB 4; Length 1117;
 Query Match
 Best Local Similarity 92.8%; Pred. No. 2.5e-54;
 Matches 324; Conservative
                           0; Mismatches
                                        25; Indels
                                                     0; Gaps
                                                               0;
         15 CGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 74
QУ
                   602 CCACCGCCGAGCCCTGGACACCAACTACTGCTTCAGCTCCACAGAAAAGAACTGCTGTGT 661
Db
         75 GCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAA 134
Qу
            662 TCGTCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAA 721
Db
        135 GGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCA 194
Oy
            722 GGGGTACCACGCCAATTTCTGCCTGGGGCCCTGCCCTTACATCTGGAGCCTGGATACACA 781
Db
        Qу
            Db
        782 GTACAGCAAGGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCTTCGGCGGCGCCCGTG 841
Qу
        255 CTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAA 314
            842 CTGCGTGCCTCAGGCGCTGGAGCCCCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAA 901
Db
        315 GGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
            902 GGTGGAGCAGTTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 950
Db
```

```
OCAF000133
LOCUS
                                         mRNA
                                                linear
                                                        MAM 06-MAY-1997
          OCAF000133
                                339 bp
DEFINITION Oryctologus cuniculus transforming growth factor beta-1 mRNA,
          partial cds.
ACCESSION
          AF000133
          AF000133.1 GI:2072531
VERSION
KEYWORDS
SOURCE
          Oryctolagus cuniculus (rabbit)
 ORGANISM
          Oryctolagus cuniculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
             (bases 1 to 339)
          Taylor, T.K., James, E.R., McGonigle, S. and Yoho, E.R.
 AUTHORS
 TITLE
          Rabbit transforming growth factor beta-1 active region
 JOURNAL
          Unpublished
REFERENCE
             (bases 1 to 339)
          Taylor, T.K., James, E.R., McGonigle, S. and Yoho, E.R.
 AUTHORS
 TITLE
          Direct Submission
 JOURNAL
          Submitted (16-APR-1997) Ophthalmology, Med. Univ. S.C., 171 Ashley
          Avenue, Charleston, SC 29464, USA
FEATURES
                  Location/Qualifiers
    source
                  1. .339
                  /organism="Oryctolagus cuniculus"
                  /mol type="mRNA"
                  /db xref="taxon:9986"
    CDS
                  <1. .339
                  /note="encodes active region"
                  /codon start=1
                  /product="transforming growth factor beta-1"
                  /protein_id="AAB53806.1"
                  /db xref="GI:2072532"
                  /translation="ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFC
                  LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
                  NMIVRSCKCS"
BASE COUNT
              71 a
                     114 c
                              97 g
                                      57 t
ORIGIN
                      85.0%; Score 308.6; DB 4; Length 339;
 Query Match
 Best Local Similarity
                      94.4%; Pred. No. 3.3e-54;
 Matches 320; Conservative
                            0; Mismatches
                                           19: Indels
                                                        0;
                                                            Gaps
                                                                   0:
Qу
         Db
          1 GCCCTGGACACCAACTACTGCTTCAGCTCCACAGAGAAGAACTGCTGTGTGCGGCAGCTG 60
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
            Db
         61 TACATTGACTTCCGCAAGGACCTGGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAC 120
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
            Db
        121 GCCAACTTCTGCCTGGGACCCTGCCCCTACATCTGGAGCCTGGACACCCAGTACAGCAAG 180
        205 GTCCTGGCTCTGTACAACCAGCACACCCGGGCGCGTCGGGCGCGCGTGCTGCGTGCCG 264
Qу
            181 GTCCTGGCCCTGTACAACCAGCACACCCGGGCGCGTCGGCAGCGCCGTGCTGTGTGCCA 240
Db
```

```
Qу
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
            Db
        241 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
        301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 15
A18277
LOCUS
          A18277
                              339 bp
                                      mRNA
                                             linear PAT 17-MAY-1994
DEFINITION H.sapiens TGF-beta 1 gene seq ID No:1.
ACCESSION
         A18277
VERSION
          A18277.1 GI:513237
KEYWORDS
SOURCE
          synthetic construct
 ORGANISM synthetic construct
          artificial sequences.
REFERENCE
            (bases 1 to 339)
 AUTHORS
          Cerletti, N., McMaster, G.K., Cox, D., Schmitz, A. and Meyhack, B.
 TITLE
          Process for the production of biologically active protein (e.g.
          TGF)
          Patent: EP 0433225-A 1 19-JUN-1991;
 JOURNAL
          CIBA-GEIGY AG
FEATURES
                 Location/Qualifiers
    source
                 1. .339
                 /organism="synthetic construct"
                 /mol type="mRNA"
                 /db xref="taxon:32630"
    CDS
                 1. .339
                 /note="Protein sequence is in conflict with the conceptual
                 translation"
                 /codon start=1
                 /transl table=11
                 /product="TGF-beta 1"
                 /protein id="CAA01385.1"
                 /db xref="GI:4529903"
                 /translation="ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFC
                 LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
                 NMIVRSCKCS"
BASE COUNT
              66 a
                    114 c
                            100 g
                                    59 t
ORIGIN
 Query Match
                     85.0%; Score 308.6; DB 6; Length 339;
 Best Local Similarity 94.4%; Pred. No. 3.3e-54;
 Matches 320; Conservative
                           0; Mismatches 19; Indels
                                                     0; Gaps
                                                                0;
Qу
         Db
          Qу
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
         61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
QУ
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
```

Db	
Qy	205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 264
Db	181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCCTGC
Qy	265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAG 324
Db	241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу	325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Db	301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339

Search completed: October 27, 2003, 18:34:44

Job time : 1417.77 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 109.057 Seconds

(without alignments)

8985.201 Million cell updates/sec

Title: US-10-017-372E-10

Perfect score: 363

Sequence: 1 gactacaaggatgacgacga.....gttcctgcaagtgcagctga 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

```
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11:
     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
12:
    /SIDS1/gcqdata/geneseg/genesegn-emb1/NA1992.DAT:*
13:
    /SIDS1/qcqdata/geneseq/qeneseqn-emb1/NA1993.DAT:*
14:
    /SIDS1/gcgdata/geneseg/genesegn-embl/NA1994.DAT:*
    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
16:
    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
17:
18:
    /SIDS1/qcqdata/qeneseq/qeneseqn-embl/NA1997.DAT:*
19:
     /SIDS1/qcqdata/qeneseq/qeneseqn-embl/NA1998.DAT:*
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
20:
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
21:
    /SIDS1/gcqdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
22:
23: /SIDS1/qcqdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
24:
    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
25:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용

Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	 339	93.4	1326	24	AAD22696	Porcine transformi
2	312.8	86.2	489	24	ABL99528	Target canine gene
3	311.8	85.9	1303	11	AAQ09317	Monkey transformin
4	311.8	85.9	1559	13	AAQ20289	Sequence encoding
5	311.8	85.9	1561	11	AAQ03268	Simian transformin
6	311.8	85.9	1571	11	AAQ03269	Human transforming
7	310.2	85.5	339	18	AAT42771	TGF-betal active f
8	310.2	85.5	339	20	AAV99375	cDNA encoding a tr
9	310.2	85.5	1560	9	AAN81084	Coding sequence of
10	310.2	85.5	1560	11	AAQ03508	Simian Transformin
11	308.6	85.0	339	17	AAT17235	Human TGF-beta 1 c
12	308.6	85.0	339	20	AAX15245	cDNA encoding the
13	308.6	85.0	650	24	ABK84023	Human cDNA differe
14	308.6	85.0	650	24	ABL68818	Kidney cancer rela
15	308.6	85.0	1176	24	ABZ35738	Human TGF beta 1 p
16	308.6	85.0	1176	24	ABX09981	Human TGFbetal DNA
17	308.6	85.0	1176	24	ABV78162	Human TGF beta 1 D
18	308.6	85.0	1176	24	ABL91703	Human polynucleoti
19	308.6	85.0	1176	25	ABV75391	TGFB1 Arg25Pro pol
20	308.6	85.0	1176	25	ABV75392	TGFB1 Arg25Pro pol
21	308.6	85.0	1569	9	AAN81085	Coding sequence of
22	308.6	85.0	1821	12	AAQ13392	Human pro-TGF-beta
23	308.6	85.Û	2537	7	AAN60972	Sequence encoding
24	308.6	85.0	2537	11	AAQ03301	cDNA encoding huma
25	308.6	85.0	2537	11	AAQ02814	Sequence of pre-TG
26	308.6	85.0	2537	15	AAQ56923	Human pre-TGF-beta
27	308.6	85.0	2537	17	AAT15720	Pre-transforming g
28	308.6	85.0	2537	19	AAV52933	Human pre-transfor
29	308.6	85.0	2742	22	AAI58342	Human polynucleoti
30	308.6	85.0	2745	16	AAT05876	cDNA encoding tran
31	308.6	85.0	2745	22	AAH28216	Nucleotide sequenc

```
Collagen Al/TGF-be
32
    308.6
            85.0
                   3541 17 AAT16516
33
    308.6
            85.0
                   3541 21 AAA12498
                                                     cDNA encoding a ch
                                                     TGFbetal 5'-UTR-CD
34
    308.6
            85.0
                   4105 15 AAQ55624
                   339 12 AAQ11993
                                                     Transforming Growt
35
      307
            84.6
                    339 17 AAT15462
                                                     Human transforming
36
      307
            84.6
                                                     Chimeric TGF-B-SA
37
      307
            84.6
                  1266 24 ABK12871
      307
                   1569 11 AAQ03509
                                                     Human Transforming
38
            84.6
      307
                   2527 25 ABQ76674
                                                     Androgen receptor
39
            84.6
                                                     Mature human Trans
40
    304.4
            83.9
                   345 14 AAQ41599
    284.8
            78.5
                   336 14 AAQ41606
                                                     Transforming Growt
41
42
    284.6
            78.4
                 1561 11 AAQ04908
                                                     Sequence encoding
                   1561 13 AAQ29177
                                                     TGF-beta 1/beta 2
    284.6
            78.4
43
                  875 23 AAS70979
    269.6
            74.3
                                                     DNA encoding novel
44
                    336 14 AAQ41604
45
    259.2
            71.4
                                                     Transforming Growt
```

ALIGNMENTS

```
RESULT 1
AAD22696
    AAD22696 standard; cDNA; 1326 BP.
ID
XX
AC
    AAD22696;
XX
DT
     26-FEB-2002 (first entry)
XX
     Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.
DE
XX
KW
     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
     diabetes mellitus; sarcoidosis; psoriasis; dermatological; ss.
KW
XX
OS
     Sus scrofa.
XX
FΗ
                     Location/Qualifiers
     Key
FT
     CDS
                     16..1188
FT
                     /*tag= a
FT
                     /product= "Porcine TGF-betal mutant protein"
XX
PN
     WO200181404-A2.
XX
PD
     01-NOV-2001.
XX
PF
     20-APR-2001; 2001WO-US12980.
XX
PR
     20-APR-2000; 2000US-199014P.
XX
PA
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PΙ
     Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
DR
     WPI; 2002-026155/03.
DR
     P-PSDB; AAE13596.
XX
PT
     Composition for treating autoimmune diseases e.g. inflammatory bowel
```

PTdisease in humans, comprises vector containing transforming growth PTfactor-beta under the control of inducible promoter XXPS Claim 1; Fig 1; 78pp; English. XXCC The invention relates to a composition containing a vector comprising a CC gene encoding a regulatory transcription factor under the control of a CC promoter encoding a transforming growth factor-beta (TGF-beta). The CC vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2 CC or TGF-beta3, its variants or homologues, by transfecting a cell which is part of a host suspected of having an autoimmune disease, especially CCCC inflammatory bowel disease (IBD), under conditions such that the CC polypeptide encoded by the nucleic acid sequence in the vector is CC expressed. The vector is delivered using a delivery system. The delivery CC of the vector results in substantial elimination of symptoms of the CCautoimmune disease and increased production of IL-10 by the host. The CC composition is useful for treating various diseases with an autoimmune CC component such as multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis CC CCand psoriasis, and also for assaying the expression of a gene in a cell. CC The vector is further useful for screening of the effect of test CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells. CC The present sequence is a cDNA encoding porcine TGF-betal mutant. XXSequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other; SO 93.4%; Score 339; DB 24; Length 1326; Query Match Best Local Similarity 100.0%; Pred. No. 8.6e-71; Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps

```
0:
Qу
      Db
      Qу
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
        910 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 969
Db
Qу
      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
        Db
      970 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1029
Qу
      205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCG 264
        1030 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGCGGCGCGCGTGCTGCGTGCCG 1089
Db
Ov
      265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
        Db
     1090 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1149
Qу
      325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
        1150 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1188
Db
```

```
ID
    ABL99528 standard; cDNA; 489 BP.
XX
AC
    ABL99528;
XX
DT
    02-JUL-2002 (first entry)
XX
DE
    Target canine gene TGFB1.
XX
KW
    Canine gene array; toxicological response; ss.
XX
OS
    Canis sp.
XX
ΡN
    WO200208453-A2.
XX
PD
    31-JAN-2002.
XX
    23-JUL-2001; 2001WO-US23311.
PF
XX
PR
    21-JUL-2000; 2000US-220057P.
XX
    (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY.
PA
XX
ΡI
    Farr SB, Pickett GG, Neft RE,
                                  Dunn RT;
XX
DR
    WPI; 2002-217063/27.
XX
PT
    Identifying toxicologically relevant canine gene to determine
PT
    toxicological responses of agents, by obtaining and comparing gene
PT
    expression profiles of untreated canine cells and canine cells treated
PT
    with an agent
XX
PS
    Disclosure; Page 67; 140pp; English.
XX
CC
    This invention relates to identifying a toxicologically relevant canine
CC
    gene and the generation of an array of toxicologically relevant
CC
    canine genes. The gene array is useful for obtaining a gene expression
CC
    profile, by exposing a population of cells to an agent, obtaining cDNA
CC
    from the population of cells, labeling the cDNA, and contacting the cDNA
CC
    with the gene array. The relevant gene is useful for making and using
CC
    arrays to determine toxicological responses to various agents, and also
CC
    useful for identifying novel gene sequences and novel canine genes.
CC
    The method for analysing toxicological responses using the canine
CC
    gene array is rapid and efficient. The present sequence is related
CC
    to the canine gene array.
XX
SQ
    Sequence 489 BP; 84 A; 183 C; 145 G; 76 T; 1 other;
 Query Match
                        86.2%; Score 312.8; DB 24; Length 489;
 Best Local Similarity
                        95.0%; Pred. No. 1.1e-64;
 Matches 323; Conservative
                              0; Mismatches
                                            17; Indels
Qу
          71 GGCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCT 130
Db
          84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
Qу
```

```
Db
        131 CTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCA 190
Qу
        144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
            Db
        191 CGCTAACTTCTGCCTGGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAA 250
        204 GGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCC 263
QУ
            Db
        264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
Qу
            311 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 370
Db
Qу
        324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
            371 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 410
Db
RESULT 3
AAQ09317
ΙD
    AAQ09317 standard; cDNA; 1303 BP.
XX
AC
    AAQ09317;
XX
DT
    25-MAR-2003 (updated)
DT
    12-AUG-1990 (first entry)
XX
DE
    Monkey transforming growth factor-beta cDNA.
XX
KW
    Transforming growth factor-beta; simian; psoriasis;
KW
    TGF-beta.
XX
OS
    Monkey.
XX
FH
    Key
                 Location/Qualifiers
FT
    sig_peptide
                 22..63
FT
                 /*tag= a
FT
    mat peptide
                 836..1170
FT
                 /*tag=b
FT
                 /product=monkey transforming growth factor-beta
XX
PN
    EP353772-A.
XX
PD
    07-FEB-1990.
XX
ΡF
    04-AUG-1989:
               89EP-0114458.
XX
PR
    05-AUG-1988;
                88US-0229133.
XX
PA
    (ONCO ) ONCOGEN LP.
XX
ΡI
    Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
DR
    WPI; 1990-038499/06.
DR
    P-PSDB; AAR03743.
XX
```

```
PT
    used to treat psoriasis by contacting cells with compositions
PT
    containing transforming growth factor-beta.
XX
    Disclosure; fig 1; 20pp; English.
PS
XX
CC
    TGF-beta may be used in the treatment of hyperplasia
CC
    associated with acanthosis-categorised skin diseases, and
CC
    in alleviating psoriatic symptoms associated with cytokine-
CC
    induced phenomena. See also AAQ03268 and AAR03750.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
    Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;
SO
 Query Match
                    85.9%; Score 311.8; DB 11; Length 1303;
                    95.0%; Pred. No. 2.3e-64;
 Best Local Similarity
 Matches 322; Conservative 0; Mismatches 17; Indels
                                                   0; Gaps
                                                            0;
        Qу
           Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           898 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 957
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           958 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1017
Db
Qу
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 264
           1018 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCG 1077
Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
       1078 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1137
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       1138 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1176
RESULT 4
AAQ20289
   AAQ20289 standard; cDNA; 1559 BP.
ΙD
XX
AC
   AAQ20289;
XX
DT
    25-MAR-2003
              (updated)
DT
    16-APR-1992
             (first entry)
XX
DE
   Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW
   Hypertension therapy; hypotensive agent; blood pressure modulator;
KW
XX
```

Inhibition of proliferation of epidermal cells -

PΤ

```
OS
    Monkey.
XX
FH
    Key
                  Location/Qualifiers
FΤ
    CDS
                  262..282
FΤ
                  /*tag=a
FT
    sig peptide
                  283..324
FT
                  /*tag=b
FT
    CDS
                  325..1098
FT
                  /*tag= c
FT
    mat peptide
                  1099..1436
FT
                  /*tag=d
XX
PN
    WO9119513-A.
XX
PD
    26-DEC-1991.
XX
PF
    20-JUN-1991;
               91WO-US04449.
XX
PR
    20-JUN-1990; 90US-0541221.
XX
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA
XX
PΙ
    Oleson FB, Comereski CR;
XX
    WPI; 1992-024199/03.
DR
DR
    P-PSDB; AAR20124.
XX
PT
    Use of transforming growth factor (TGF)-beta and their
PT
    antagonists - for modulating blood pressure, for treating
PT
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CC
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
    (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SO
    Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;
 Query Match
                      85.9%; Score 311.8; DB 13; Length 1559;
 Best Local Similarity 95.0%; Pred. No. 2.3e-64;
 Matches 322; Conservative
                            0; Mismatches 17; Indels
                                                        0; Gaps
                                                                  0;
Qу
         Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
            1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
```

```
Db
       1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
        Qy
            Db
       1275 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCGTGCCG 1334
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
            Db
       1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
            Db
       1395 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1433
RESULT 5
AAQ03268
ID
    AAQ03268 standard; DNA; 1561 BP.
XX
AC
    AAQ03268;
XX
DT
    25-MAR-2003
               (updated)
DT
    12-AUG-1990 (first entry)
XX
DE
    Simian transforming growth factor-beta cDNA.
XX
KW
    Transforming growth factor-beta; psoriasis; TGF-beta; ss.
XX
OS
    Monkey.
XX
FH
    Key
                 Location/Qualifiers
FT
                 283..324
    sig peptide
FT
                 /*tag= a
FT
    mat peptide
                 1096..1431
FT
                 /*tag=b
FT
                 /product=human transforming growth factor-beta
XX
PN
    EP353772-A.
XX
PD
    07-FEB-1990.
XX
PF
    04-AUG-1989; 89EP-0114458.
XX
PR
    05-AUG-1988; 88US-0229133.
XX
    (ONCO ) ONCOGEN LP.
PA
XX
    Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
PΙ
XX
DR
    WPI; 1990-038499/06.
DR
    P-PSDB; AAR03743.
XX
PT
    Inhibition of proliferation of epidermal cells -
PT
    used to treat psoriasis by contacting cells with compositions
PT
    containing transforming growth factor-beta.
XX
```

```
XX
CC
   TGF-beta may be used in the treatment of hyperplasia
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
   induced phenomena. See also AAQ03269 and AAR03750.
CC
   (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
   Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
 Query Match
                  85.9%; Score 311.8; DB 11; Length 1561;
 Best Local Similarity
                  95.0%; Pred. No. 2.3e-64;
 Matches 322; Conservative 0; Mismatches
                                  17; Indels
                                             0; Gaps
                                                     0:
       Qу
          Db
      Qу
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
         1156 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCCAAGGGCTACCAT 1215
Db
      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
      1216 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1275
       Qу
          Db
      265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          1336 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1395
Db
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
         Db
      1396 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1434
RESULT 6
AAQ03269
ΙD
   AAQ03269 standard; DNA; 1571 BP.
XX
AC
   AAQ03269;
XX
DT
   25-MAR-2003
            (updated)
DT
   12-AUG-1990
            (first entry)
XX
DΕ
   Human transforming growth factor-beta cDNA.
XX
KW
   Transforming growth factor-beta; psoriasis;
   TGF-beta.
KW
XX
0S
   Homo sapiens.
XX
FH
   Key
              Location/Oualifiers
              22..63
FT
   sig peptide
```

PS

Disclosure; fig 1; 20pp; English.

```
FT
                /*tag= a
FT
                836..1170
   mat peptide
FT
                /*tag= b
                /product=human transforming growth factor-beta
FT
XX
PN
   EP353772-A.
XX
PD
   07-FEB-1990.
XX
PF
   04-AUG-1989;
               89EP-0114458.
XX
PR
   05-AUG-1988;
               88US-0229133.
XX
    (ONCO ) ONCOGEN LP.
PA
XX
PΙ
   Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
DR
   WPI; 1990-038499/06.
DR
   P-PSDB; AAR03750.
XX
PT
   Inhibition of proliferation of epidermal cells -
PT
   used to treat psoriasis by contacting cells with compositions
PT
   containing transforming growth factor-beta.
XX
PS
   Disclosure; fig 1; 20pp; English.
XX
CC
   TGF-beta may be used in the treatment of hyperplasia
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
    induced phenomena. See also AAQ03268 and AAR03743.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
   Sequence 1571 BP; 299 A; 563 C; 443 G; 266 T; 0 other;
                    85.9%; Score 311.8; DB 11; Length 1571;
 Best Local Similarity
                    95.0%; Pred. No. 2.3e-64;
                        0; Mismatches 17; Indels
 Matches 322; Conservative
                                                  0; Gaps
                                                           0:
Qу
        Dh
Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           1166 TATATTGACTTCCGCAAGGACCTCGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1225
Db
QУ
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
           1226 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1285
Dυ
Qу
       1286 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCGTGCCG 1345
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           1346 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1405
Db
```

```
Qу
          325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
              1406 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGCTGA 1444
Db
RESULT 7
AAT42771
ΙD
     AAT42771 standard; cDNA; 339 BP.
XX
AC
     AAT42771;
XX
DT
     26-AUG-1997 (first entry)
XX
DE
     TGF-betal active fragment of a TGF-beta fusion protein encoding cDNA.
XX
KW
     Transforming growth factor-beta fusion protein; wound healing;
KW
     artificial skin; surgery recovery time; ss.
XX
OS
     Homo sapiens.
XX
FΗ
                    Location/Qualifiers
     Key
FT
     CDS
                     1..339
FT
                     /*tag= a
FT
                     /function= TGF active fragment
XX
PN
     WO9639430-A1.
XX
PD
     12-DEC-1996.
XX
ΡF
     05-JUN-1996;
                  96WO-US08973.
XX
PR
     06-JUN-1995; 95US-0470837.
XX
PΑ
     (CHEU/) CHEUNG D T.
PΑ
     (HALL/) HALL F L.
PA
     (NIMN/) NIMNI M E.
PA
     (TUAN/) TUAN T.
     (WULL/) WU L.
PA
XX
ΡI
     Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX
DR
    WPI; 1997-043065/04.
DR
     P-PSDB; AAW08173.
XX
PT
     Prepn. of transforming growth factor-beta fusion protein - useful to
PT
     reduce surgery recovery time and to prepare artificial skin
XX
PS
     Disclosure; Page 44-45; 59pp; English.
XX
    A novel transforming growth factor-beta (TGF-beta) fusion protein
CC
CC
     comprises a purification tag and a TGF active fragment. The present
CC
     sequence encodes a specifically claimed TGF active fragment, TGF-beta1.
CC
     Additionally, the fusion protein may comprise proteinase-sensitive
     linker sites and binding domain so the protein sequence may contain
CC
     some or all of the following elements: purification tag:proteinase
CC
```

site: ECM binding site: proteinase site: TGF-beta. TGF-beta promotes

CC

```
CC
    wound healing, and the fusion protein can be used to reduce surgery
CC
    recovery time and in the preparation of artificial skin. The inclusion
CC
    of a purification tag facilitates purification of the fusion protein.
CC
    The proteinase site is included to permit cleavage and release of the
CC
    purification tag after purification if desired. The extracellular
CC
    matrix binding site facilitates delivery of the fusion protein to the
CC
    desired site of action. Delivery of the TGF-beta to the site to be
CC
    treated reduces the amount of TGF-beta required to be administered to
CC
    be effective and reduces the concentration of circulating TGF-beta
CC
    which may result in undesirable effects.
XX
SO
    Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;
 Query Match
                     85.5%; Score 310.2; DB 18; Length 339;
 Best Local Similarity 94.7%; Pred. No. 4.4e-64;
 Matches 321; Conservative
                         0; Mismatches
                                        18; Indels
                                                     0; Gaps
                                                               0;
Qу
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Dh
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCG 264
Qу
            181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCTGCTGCCGCCCC 240
Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
        241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
        301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 8
AAV99375
ID
    AAV99375 standard; cDNA; 339 BP.
XX
AC
    AAV99375;
XX
DT
    25-MAR-1999 (first entry)
XX
DE
    cDNA encoding a transforming growth factor beta active fragment.
XX
KW
    Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW
    bone morphogenetic protein; transforming growth factor beta:
    active fragment; wound healing; bone growth; purification tag; ds.
KW
XX
OS
    Homo sapiens.
```

```
XX
PN
    WO9855137-A1.
XX
PD
    10-DEC-1998.
XX
PF
    02-JUN-1998; 98WO-US11189.
XX
PR
    03-JUN-1997; 97US-0868452.
XX
PA
    (HALL/) HALL F L.
PΑ
    (HANB/) HAN B.
PΑ
    (NIMN/) NIMNI M E.
PA
    (SHOR/) SHORS E C.
    (WULL/) WU L.
PA
XX
ΡI
    Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX
DR
    WPI; 1999-059875/05.
DR
    P-PSDB; AAW84207.
XX
PT
    New bone morphogenetic fusion proteins - comprising a purification
PT
    tag and a bone morphogenetic active fragment, used for enhancing
PT
    wound healing or bone growth
XX
PS
    Example 1; Page 41; 64pp; English.
XX
CC
    The present sequence encodes a transforming growth factor beta active
CC
    fragment. The protein can be used in place of a bone morphogenetic
CC
    active fragment to create the fusion proteins of the invention. When a
CC
    bone morphogenetic active fragment is used, the fusion proteins are
    designated bone morphogenetic fusion proteins. The bone morphogenetic
CC
CC
    fusion protein may contain some or all of the following elements: a
CC
    purification tag, a proteinase site, an ECM/bone binding site, a second
CC
    proteinase site, and a bone morphogenetic protein active fragment.
CC
    The bone morphogenetic fusion proteins can be used for enhancing wound
CC
    healing or bone growth.
XX
    Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;
SO
 Query Match
                     85.5%; Score 310.2; DB 20; Length 339;
 Best Local Similarity
                     94.7%; Pred. No. 4.4e-64;
 Matches 321; Conservative
                           0; Mismatches
                                         18; Indels
                                                      0; Gaps
                                                                0;
Qу
         Db
          Qу
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
            Db
         61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
            121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCGTCCCG 264
Qу
```

```
Db
         181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCGC 240
Qу
         265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
             Db
         241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Qу
         325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
             Db
         301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 9
AAN81084
ID
    AAN81084 standard; cDNA; 1560 BP.
XX
AC
    AAN81084;
XX
DT
    25-MAR-2003
                 (updated)
    09-OCT-1990 (first entry)
DT
XX
DE
    Coding sequence of simian transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS
    Cercopithecus aethiops.
XX
FH
                   Location/Qualifiers
    Key
FT
                   261..1433
    CDS
FT
                    /*taq=a
FT
                   282..323
    sig_peptide
FT
                    /*tag= b
FT
                    1095..1433
    mat peptide
FT
                    /*tag= c
XX
PN
    EP293785-A.
XX
PD
    07-DEC-1988.
XX
PF
    27-MAY-1988;
                 88EP-0108528.
XX
PR
    29-MAY-1987;
                 87US-0055662.
PR
    25-JAN-1988;
                  88US-0147842.
XX
PA
     (ONCO ) ONCOGEN.
PA
     (BRIM ) BRISTOL-MYERS CO.
XX
PI
    Purchio AG, Gentry L, Twardzik D;
XX
DR
    WPI; 1988-347488/49.
    P-PSDB; AAP80647.
DR
XX
PT
    Prodn. of simian transforming growth factor beta-1 - by culturing
PT
    transfected eucaryotic cells, and new precursor proteins, useful for
PT
    treating tumours.
XX
PS
    Disclosure; Page ?; pp; English.
```

XX

```
The cDNA is prepd. from African green monkey cell line BSC-40 and is
CC
    expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC
    between mature simian and human TGF-beta 1. The plasmid also contains
CC
    the SV40 promoter and a selection marker, esp. DHFR.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
CC
    (Updated on 25-MAR-2003 to correct PI field.)
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
 Query Match
                   85.5%; Score 310.2; DB 9; Length 1560;
 Best Local Similarity 94.7%; Pred. No. 5.6e-64;
 Matches 321; Conservative 0; Mismatches
                                    18;
                                        Indels
                                                0; Gaps
                                                         0;
Qу
        Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          Db
      1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
      1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
       205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCG 264
Qу
          Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAG 324
Qу
           Db
      1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
Qу
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
          Db
      1395 CTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433
RESULT 10
AA003508
ID
   AAQ03508 standard; DNA; 1560 BP.
XX
AC
   AAQ03508;
XX
DT
   25-MAR-2003
             (updated)
DT
   09-JAN-2003
             (updated)
DT
   14-AUG-1990
             (first entry)
XX
DE
   Simian Transforming growth factor - Betal.
XX
   HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW
KW
   factors; ds.
XX
OS
   Cebus apella.
XX
FΗ
   Key
               Location/Qualifiers
               267..1437
FT
   CDS
```

CC

```
FT
                /*tag=a
FT
   mat peptide
               1103..1437
FT
                /*tag= b
XX
PN
   EP356935-A.
XX
   07-MAR-1990.
PD
XX
ΡF
   25-AUG-1989;
             89EP-0115719.
XX
             88US-0236698.
PR
   25-AUG-1988:
XX
   (ONCO ) ONCOGEN LP.
PΑ
XX
PΙ
   Brankovan V, Lioubin M, Purchio A;
XX
   WPI; 1990-068723/10.
DR
DR
   P-PSDB; AAR05663.
XX
PT
   Compsns. contg. transforming growth factor beta -
   used for inhibitions of HIV infection and replication in vivo.
PT
XX
PS
   Disclosure; Fig 1; 20pp; English.
XX
CC
   TGF-beta may be used in vivo to prevent formation of synctia and
   inhibit HIV infection. TGF may also be used with other HIV treatments
CC
CC
   (AZT, soluble CD4 etc.).
CC
    (Updated on 09-JAN-2003 to add missing OS field.)
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                   85.5%; Score 310.2; DB 11; Length 1560;
 Best Local Similarity 94.7%; Pred. No. 5.6e-64;
 Matches 321; Conservative 0; Mismatches 18; Indels
                                                0; Gaps
Qу
        Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          Db
      1155 TATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1214
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          1215 GCCAACTTCTGCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1274
Db
Qу
       Db
      1275 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCG 1334
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
      1335 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1394
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
```

1395 CTGTCCAACATGATCGTGCGCTCCTGAAAATGCAGCTGA 1433 RESULT 11

```
AAT17235
ΙD
    AAT17235 standard; cDNA to mRNA; 339 BP.
XX
AC
    AAT17235;
XX
DT
     17-JUL-1996 (first entry)
XX
DE
    Human TGF-beta 1 cDNA.
XX
KW
    Transforming growth factor type beta; TGF-beta 1;
KW
    protein renaturation; protein folding; ds.
XX
OS
    Homo sapiens.
XX
PN
    WO9603433-A1.
XX
PD
     08-FEB-1996.
XX
PF
    12-JUL-1995;
                  95WO-EP02719.
XX
PR
    25-JUL-1994;
                  94EP-0810439.
XX
     (CIBA ) CIBA GEIGY AG.
PA
XX
PΙ
    Cerletti N;
XX
DR
    WPI; 1996-117000/12.
DR
     P-PSDB; AAR92773.
XX
PT
     Prodn. of dimeric biologically active transforming growth factor -
PT
    by refolding denatured monomer in detergent-free folding buffer
PT
    contg. specific organic solvent to improve yield
XX
PS
    Example 1B; Page 20-30; 54pp; English.
XX
CC
    The coding sequence (AAT17235) of human transforming growth factor
CC
    TGF-beta 1 (AAR92773) was cloned into plasmid pGEM-5ZF(+) (Promega)
CC
    and the construct used to transform E. coli Y1090. Subcloning in
CC
    pPLMu yielded plasmid pPLMu.hTGF-beta 1. Non-soluble, monomeric
    TGF-beta 1 was recovered from E. coli LC 137/pPLMu.hTGF-beta 1 (DSM
CC
CC
    5656) transformants. A biologically active, dimeric form of
    TGF-beta 1 was obtd. by refolding this monomer in detergent-free
CC
CC
    buffer contg. DMSO and/or DMF. Dimers of TGF-beta 3 (AAR92772) and
CC
    TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were
CC
    also produced.
XX
    Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other;
SO
 Query Match
                          85.0%; Score 308.6; DB 17; Length 339;
                         94.4%; Pred. No. 1.1e-63;
 Best Local Similarity
 Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps
```

0;

```
Qу
          Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          11]]}}|
Db
        61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
       Qу
       Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Db
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
          Db
       301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 12
AAX15245
ΙD
   AAX15245 standard; cDNA; 339 BP.
XΧ
AC
   AAX15245;
XX
DT
   20-MAR-2003 (updated)
DT
   28-APR-1999 (first entry)
XX
DE
   cDNA encoding the mature form of transforming growth factor-beta-1.
XX
KW
   Transforming growth factor-beta-1; TGF-beta-like protein;
KW
   S-sulphonated TGF-beta-like protein; wound treatment; cancer;
KW
   bone repair; tissue repair; bone marrow protective agent;
KW
   cardioprotection; anti-inflammatory; immunosuppressive;
KW
   ulcer; bed sore; ds.
XX
OS
   Homo sapiens.
XX
PN
   EP891985-A1.
XX
PD
   20-JAN-1999.
XX
PF
   27-NOV-1990;
             98EP-0113487.
XX
PR
   06-DEC-1989;
              89GB-0027546.
PR
   27-NOV-1990;
              90EP-0810922.
XX
   (NOVS ) NOVARTIS AG.
PΑ
XX
PΙ
   Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX
```

```
DR
    WPI; 1999-083520/08.
DR
    P-PSDB; AAW97091.
XX
PΤ
    Producing biologically active dimeric Transforming Growth
PT
    Factor-beta - by refolding new monomeric Transforming Growth
PT
    Factor-beta, useful for treatment of wounds and cancer
XX
PS
    Example 1; Page 28; 32pp; English.
XX
CC
    The present sequence encodes the mature form of transforming growth
CC
    factor-beta-1. Dimeric, biologically active TGF-beta-like protein
CC
    can be produced by subjecting the denatured monomeric form to refolding
CC
    conditions. The new monomeric S-sulphonated TGF-beta-like protein is
CC
    useful for the production of the dimeric, biologically active
CC
    TGF-beta-like protein, which is useful for the treatment of wounds
CC
    (surface or internal) and cancer in a mammal, in bone and tissue
CC
    repair, as a bone marrow protective agent, a mediator of
CC
    cardioprotection, for the production of an anti-inflammatory or
CC
    immunosuppressive preparation. Treatment is useful for animals,
CC
    especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
CC
    particularly useful for the elderly.
CC
    (Updated on 20-MAR-2003 to correct PF field.)
CC
    (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ
    Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other;
 Query Match
                     85.0%; Score 308.6; DB 20; Length 339;
 Best Local Similarity
                     94.4%; Pred. No. 1.1e-63;
 Matches 320; Conservative
                           0; Mismatches
                                        19: Indels
                                                               0:
Qу
         Db
         Qу
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
         61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTGGCGGCGCGTGCTGCGTGCCG 264
Qу
           181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCG 240
Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
        241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
Db
```

```
ID
     ABK84023 standard; cDNA; 650 BP.
XX
AC
     ABK84023;
XX
DT
     14-AUG-2002 (first entry)
XX
DΕ
     Human cDNA differentially expressed in granulocytic cells #594.
XX
KW
     Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW
     viral infection; parasitic infection; protozoal infection;
KW
     fungal infection; sterile inflammatory disease; psoriasis;
KW
     rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
     cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW
KW
     adult respiratory distress syndrome; inflammatory bowel disease;
KW
     Crohn's disease; ulcerative colitis; periodontal disease;
KW
     granulocyte activation; chronic inflammation; allergy.
XX
OS
     Homo sapiens.
XX
PN
     WO200228999-A2.
XX
PD
     11-APR-2002.
XX
PF
     03-OCT-2001; 2001WO-US30821.
XX
PR
     03-OCT-2000; 2000US-237189P.
XX
PA
     (GENE-) GENE LOGIC INC.
XX
PΙ
     Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR
     WPI; 2002-435328/46.
XX
PT
     Detecting granulocyte activation by detecting differential expression
PT
     of genes associated with granulocyte activation, which serves as
PT
     diagnostic markers that is useful for monitoring disease states and
PT
     drug toxicity
XX
PS
     Claim 1; SEQ ID No 594; 114pp; English.
XX
CC
     The invention relates to detecting (M1) granulocyte (GC) activation
CC
     (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC
     DNA chip analysis as given in the specification, and comparing
CC
     the expression level to an expression level in an unactivated
CC
     GC, where differential expression of Gs is indicative of GCA.
CC
     Also included are modulating (M2) GA by contacting GC with an agent
CC
     that alters the expression of at least one gene in Gs; (2) screening (M3)
CC
     for an agent capable of modulating GCA or an inflammation (especially
     chronic) in a tissue, an allergic response in a subject, exposure of a
CC
CC
     subject to a pathogen or sterile inflammatory disease using the
CC
     gene expression profile; (3) detecting (M4) an inflammation (especially
     chronic) in a tissue, an allergic response in a subject, exposure of a
CC
CC
     subject to a pathogen or sterile inflammatory disease, by detecting the
CC
     level of expression in a sample of the tissue of gene(s) from Gs, where
CC
     the level of expression of the gene is indicative of inflammation;
CC
     (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC
     an allergic response in a subject, exposure of a subject to a pathogen
```

```
CC
    or sterile inflammatory disease, by contacting a tissue having
CC
    inflammation with an agent that modulates the expression of gene(s)
CC
    from Gs in the tissue. Ml is useful for detecting GCA; M2 is useful for
CC
    modulating GA; M3 is useful for screening an agent capable of modulating
CC
    GCA preferably in an inflammation in a tissue; M4 is useful for
CC
    detecting an inflammation (especially chronic) in a tissue, an allergic
CC
    response in a subject, exposure of a subject to a pathogen or sterile
CC
    inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC
    glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
    reperfusion injury, ARDS, adult respiratory distress syndrome,
CC
CC
    inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC
    periodontal disease; also bacterial infection, viral infection,
CC
    parasitic infection, protozoal infection, fungal infection and M5 is
CC
    useful for treating one of the above conditions. The present
CC
    sequence represents a gene differentially expressed in granulocytes.
CC
    Note: The sequence data for this patent did not form part
CC
    of the printed specification, but was obtained in electronic
CC
    format directly from WIPO at
CC
    ftp.wipo.int/pub/published pct sequences.
XX
    Sequence 650 BP; 108 A; 244 C; 179 G; 119 T; 0 other;
SO
 Query Match
                    85.0%; Score 308.6; DB 24; Length 650;
 Best Local Similarity
                    94.4%; Pred. No. 1.2e-63;
                         0; Mismatches
 Matches 320; Conservative
                                      19; Indels
                                                   0;
                                                      Gaps
                                                            0;
Qу
        Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
Db
        Qу
           Db
Qу
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
           241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Db
Qу
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
ďū
RESULT 14
ABL68818
ID
    ABL68818 standard; DNA; 650 BP.
XX
AC
   ABL68818;
XX
```

```
DT
     15-MAY-2002 (first entry)
XX
DE
     Kidney cancer related gene sequence SEQ ID NO:7155.
XX
KW
     Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW
     stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW
     cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW
     gene; ds.
XX
OS
     Homo sapiens.
XX
PN
     WO200194629-A2.
XX
PD
     13-DEC-2001.
XX
PF
     30-MAY-2001; 2001WO-US10838.
XX
PR
     05-JUN-2000; 2000US-209473P.
PR
     05-JUN-2000; 2000US-209531P.
PR
     18-SEP-2000; 2000US-233133P.
PR
     18-SEP-2000; 2000US-233617P.
PR
     20-SEP-2000; 2000US-234009P.
PR
     20-SEP-2000; 2000US-234034P.
     20-SEP-2000; 2000US-234052P.
PR
PR
     22-SEP-2000; 2000US-234509P.
     22-SEP-2000; 2000US-234567P.
PR
     25-SEP-2000; 2000US-234923P.
PR
PR
     25-SEP-2000; 2000US-234924P.
PR
     25-SEP-2000; 2000US-235077P.
PR
     25-SEP-2000; 2000US-235082P.
PR
     25-SEP-2000; 2000US-235134P.
PR
     25-SEP-2000; 2000US-235280P.
PR
     26-SEP-2000; 2000US-235637P.
     26~SEP-2000; 2000US-235638P.
PR
     27-SEP-2000; 2000US-235711P.
PR
PR
     27-SEP-2000; 2000US-235720P.
PR
     27-SEP-2000; 2000US-235840P.
PR
     27-SEP-2000; 2000US-235863P.
PR
     28-SEP-2000; 2000US-236028P.
PR
     28-SEP-2000; 2000US-236032P.
PR
     28-SEP-2000; 2000US-236033P.
     28-SEP-2000; 2000US-236034P.
PR
     28-SEP-2000; 2000US-236109P.
PR
PR
     28-SEP-2000; 2000US-236111P.
PR
     29-SEP-2000; 2000US-236842P.
PR
     29-SEP-2000; 2000US-236891P.
PR
     02-OCT-2000; 2000US-237172P.
PR
     02-OCT-2000; 2000US-237173P.
PR
     02-OCT-2000; 2000US-237278P.
     02-OCT-2000; 2000US-237294P.
PR
     02-OCT-2000; 2000US-237295P.
PR
     02-OCT-2000; 2000US-237316P.
PR
PR
     03-OCT-2000; 2000US-237425P.
PR
     03-OCT-2000; 2000US-237598P.
     03-OCT-2000; 2000US-237604P.
PR
PR
     03-OCT-2000; 2000US-237606P.
```

PR

03-OCT-2000; 2000US-237608P.

```
PR
    01-NOV-2000: 2000US-244867P.
PR
    01-NOV-2000; 2000US-245084P.
XX
PΑ
    (AVAL-) AVALON PHARM.
XX
ΡI
    Young PE, Augustus M,
                        Carter KC, Ebner R,
                                           Endress G, Horrigan S;
ΡI
    Soppet DR, Weaver Z;
XX
DR
    WPI; 2002-188264/24.
XX
\mathbf{PT}
    Screening for anti-neoplastic agent involves exposing cells to a
PΤ
    chemical agent to be tested for anti-neoplastic activity, and
PΤ
    determining a change in expression of a gene of a signature gene set -
XX
PS
    Claim 1; SEQ ID 7155; 44pp; English.
XX
CC
    The present invention describes a method (M1) for screening for an
CC
    anti-neoplastic agent. The method involves exposing cells to a chemical
CC
    agent to be tested for anti-neoplastic activity, determining a change in
CC
    expression of at least one gene (I) of a signature gene set, where (I)
CC
    comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC
    to ABL70110), or is at least 95% identical to (S), where a change in
CC
    expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC
    activity and can be used in gene therapy. M1 can be used for screening
CC
    an anti-neoplastic agent, and can be used for producing a product which
    is the data collected with respect to the anti-neoplastic agent as a
CC
CC
    result of M1, and the data is sufficient to convey the chemical
CC
    structure and/or properties of the agent. M1 can be used in the
CC
    treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC
    oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC
    adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC
    infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC
    carcinoma, papillary carcinoma and Wilm's tumour.
XX
SO
    Sequence 650 BP; 108 A; 244 C; 179 G; 119 T; 0 other;
                      85.0%; Score 308.6; DB 24; Length 650;
 Query Match
 Best Local Similarity
                      94.4%; Pred. No. 1.2e-63;
 Matches 320; Conservative 0; Mismatches
                                         19; Indels
                                                       0; Gaps
                                                                 0;
QУ
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Ov
            61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
            Db
        121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
QУ
        Db
        181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCGCCGCCA
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
```

```
Db
          241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
          325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
              Db
          301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 15
ABZ35738
    ABZ35738 standard; DNA; 1176 BP.
XX
AC
    ABZ35738;
XX
DT
     07-FEB-2003 (first entry)
XX
DE
     Human TGF beta 1 polynucleotide SEQ ID NO 46.
XX
KW
     Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KW
    protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
     virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KW
KW
     Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS
    Homo sapiens.
XX
PN
    DE10100588-A1.
XX
PD
    18-JUL-2002.
XX
ΡF
     09-JAN-2001; 2001DE-1000588.
XX
PR
     09-JAN-2001; 2001DE-1000588.
XX
PA
     (RIBO-) RIBOPHARMA AG.
XX
ΡI
    Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
    WPI; 2002-683450/74.
DR
XX
PT
    Inhibiting expression of target genes, useful e.g. for treating tumors,
PT
    by introducing into cells two double-stranded RNAs that are
PT
    complementary to the target -
XX
PS
    Claim 13; Page 34-35; 100pp; German.
XX
CC
    The invention relates to inhibiting expression of a target gene in a cell
CC
    by introducing at least two oligoribonucleotides (dsRNAI and II), both
CC
    with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC
    pairs. At least part of one strand (S1, S2) of the ds structures in each
CC
    of dsRNAI and II are complementary to regions in the target gene. The
CC
    method uses antisense inhibition of gene expression using double stranded
CC
    RNA inhibition (RNAi). The method is particularly used to treat tumours
CC
    or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC
    humans, animals or plants). The method provides more effective inhibition
CC
    of expression than known methods using a single dsRNA, even at very low
CC
    concentrations. When dsRNA has at least one unpaired nucleotide at the
CC
    end, stability (and thus effective concentration in the cell) is
```

```
CC
   improved and efficiency can be increased further by pretreating the cells
CC
   with interferon. The present sequence is that of a target DNA of the
CC
   invention.
XX
SO
   Sequence 1176 BP; 239 A; 382 C; 353 G; 202 T; 0 other;
 Query Match
                 85.0%; Score 308.6; DB 24; Length 1176;
 Best Local Similarity
                 94.4%; Pred. No. 1.3e-63;
 Matches 320; Conservative
                    0: Mismatches
                               19; Indels
                                          0; Gaps
                                                  0;
       Qу
         Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
         Db
      898 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 957
      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
         Db
      958 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1017
      Qу
         1018 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCGTGCCG 1077
Db
Qу
      265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
         Db
     1078 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1137
      325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
         Db
     1138 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1176
```

Search completed: October 27, 2003, 19:10:54 Job time: 110.057 secs

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 18:35:27; Search time 107.894 Seconds

(without alignments)

9022.658 Million cell updates/sec

Title: US-10-017-372E-10

Perfect score: 363

Sequence: 1 gactacaaggatgacgacga.....gttcctgcaagtgcagctga 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 segs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:* 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:* 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:* 4: /cgn2 6/ptodata/2/pubpna/US06_PUBCOMB.seq:* 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:* 6: /cgn2_6/ptodata/2/pubpna/PCTUS PUBCOMB.seq:* 7: /cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:* 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:* 9: /cgn2 6/ptodata/2/pubpna/US09A PUBCOMB.seg:* 10: /cgn2 6/ptodata/2/pubpna/US09B PUBCOMB.seg:* 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:* 12: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seg:* 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:* 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:* 15: /cgn2 6/ptodata/2/pubpna/US10 NEW PUB.seg:* 16: /cgn2 6/ptodata/2/pubpna/US60 NEW PUB.seg:* 17: /cgn2 6/ptodata/2/pubpna/US60 PUBCOMB.seg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	312.8	86.2	489	11	US-09-911-904-167	Sequence 167, App
2	308.6	85.0	339	10	US-09-813-271B-1	Sequence 1, Appli
3	308.6	85.0	1821	14	US-10-087-268-1	Sequence 1, Appli
4	308.6	85.0	1821	14	US-10-087-268-4	Sequence 4, Appli
5	308.6	85.0	2742	14	US-10-037-270-220	Sequence 220, App
6	308.6	85.0	2745	11	US-09-948-002-28	Sequence 28, Appl
7	287.8	79.3	1585	11	US-09-948-002-27	Sequence 27, Appl
8	287.8	79.3	2094	11	US-09-948-002-1	Sequence 1, Appli
9	227.2	62.6	336	10	US-09-813-271B-7	Sequence 7, Appli
10	211.2	58.2	2879	11	US-09-906-158-10	Sequence 10, Appl
11	211.2	58.2	4382	12	US-09-957-458B-9	Sequence 9, Appli
12	210.4	58.Û	2574	11	US-09-906-158-3	Sequence 3, Appli
13	210.4	58.0	2574	13	US-10-028-158-20	Sequence 20, Appl
14	209.4	57.7	339	10	US-09-813-271B-5	Sequence 5, Appli
15	182.4	50.2	336	10	US-09-813-271B-11	Sequence 11, Appl
16	180.8	49.8	336	10	US-09-813-271B-9	Sequence 9, Appli
17	166.2	45.8	4267	11	US-09-948-002-47	Sequence 47, Appl
18	158.2	43.6	339	10	US-09-813-271B-3	Sequence 3, Appli
19	158.2	43.6	2570	12	US-09-960-706-663	Sequence 663, App
20	158.2	43.6	2912	13	US-10-044-090-323	Sequence 323, App

```
Sequence 15319, A
  21
        141.6
                39.0
                        597 9
                               US-09-864-761-15319
c 22
        134.8
                37.1
                        154
                            9 US-09-864-761-31841
                                                           Sequence 31841, A
                                                            Sequence 577, App
С
  23
        131.8
                36.3
                        206
                                US-09-833-381-577
                            10
   24
        104.8
                28.9
                        851
                            13
                                US-10-027-632-152938
                                                            Sequence 152938,
   25
                28.0 29000
        101.6
                            11
                                 US-09-906-158-17
                                                            Sequence 17, Appl
   26
        100.4
                27.7
                        224
                                 US-09-833-381-73
                                                            Sequence 73, Appl
                             10
   27
         73.2
                20.2
                        450
                            11
                                 US-09-918-995-6145
                                                            Sequence 6145, Ap
С
  28
         69.4
                19.1
                        176 10
                                 US-09-833-381-571
                                                            Sequence 571, App
   29
           69
                19.0
                        584
                            12
                                US-10-029-386-9758
                                                            Sequence 9758, Ap
   30
         68.2
                18.8
                        176 12
                                 US-10-029-386-23458
                                                            Sequence 23458, A
   31
         57.4
                15.8
                        486 11
                                 US-09-918-995-25641
                                                            Sequence 25641, A
   32
         48.6
                13.4
                        557 9 US-09-765-527-248
                                                           Sequence 248, App
   33
         48.6
                13.4
                        557
                            9 US-09-760-397-1
                                                           Sequence 1, Appli
   34
         48.6
                13.4
                        557
                            12 US-10-324-182-1
                                                            Sequence 1, Appli
   35
         48.6
                13.4
                        610
                            9 US-09-760-397-7
                                                           Sequence 7, Appli
   36
         48.6
                13.4
                        610 12 US-10-324-182-7
                                                            Sequence 7, Appli
   37
         48.6
               13.4
                        613 9 US-09-765-527-256
                                                           Sequence 256, App
   38
         48.6
               13.4
                        613 9 US-09-765-527-260
                                                           Sequence 260, App
   39
         48.6
               13.4
                        646 9 US-09-760-397-13
                                                           Sequence 13, Appl
   40
         48.6
               13.4
                        646 12 US-10-324-182-13
                                                            Sequence 13, Appl
   41
         48.6
                        658 9 US-09-765-527-254
                13.4
                                                           Sequence 254, App
   42
                        661 9 US-09-765-527-262
         48.6
                13.4
                                                           Sequence 262, App
   43
         48.6
                13.4
                       1004 8
                               US-08-957-425-10
                                                           Sequence 10, Appl
   44
         48.6
                13.4
                       1277 8 US-08-957-425-14
                                                           Sequence 14, Appl
   45
         48.6
               13.4
                       1505 8 US-08-957-425-12
                                                           Sequence 12, Appl
```

ALIGNMENTS

```
RESULT 1
US-09-911-904-167
; Sequence 167, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
  APPLICANT: Farr, Spencer B.
  APPLICANT:
              Pickett, Gavin G.
   APPLICANT:
              Neft, Robin Eileen
  APPLICANT:
              Dunn, II, Robert Thomas
   TITLE OF INVENTION: CANINE TOXICITY GENES
  FILE REFERENCE: 400742000200
   CURRENT APPLICATION NUMBER: US/09/911,904
   CURRENT FILING DATE: 2002-04-09
   PRIOR APPLICATION NUMBER: US 60/220,057
   PRIOR FILING DATE: 2000-07-21
   NUMBER OF SEQ ID NOS: 386
   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
    LENGTH: 489
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: misc feature
    LOCATION: (1)...(489)
    OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167
```

```
Best Local Similarity
                    95.0%; Pred. No. 2.9e-84;
 Matches 323; Conservative
                          0; Mismatches 17; Indels
                                                    0; Gaps
                                                              0;
Qу
         Db
         71 GGCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCT 130
         84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
Qу
           131 CTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCA 190
Db
        144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
Qу
            Db
        191 CGCTAACTTCTGCCTGGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAA 250
        204 GGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCC 263
Qу
           Db
        251 GGTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCC 310
        264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
Qу
           Db
        311 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 370
        324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           371 GCTGTCGAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 410
Dh
RESULT 2
US-09-813-271B-1
; Sequence 1, Application US/09813271B
 Patent No. US20020115834A1
   GENERAL INFORMATION:
       APPLICANT:
                (A) Nico Cerletti
       TITLE OF INVENTION: New process for the production of
                       biologically active protein
       NUMBER OF SEQUENCES: 13
       CORRESPONDENCE ADDRESS:
           ADDRESSEE: No. US20020115834Alartis Patent Department
           STREET: 564 Morris Avenue
           CITY: Summit
           STATE: New Jersey
           COUNTRY: USA
           ZIP: 07901
       COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/813,271B
           FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: PCT/EP95/02719
           FILING DATE: 12-Jul-95
```

86.2%; Score 312.8; DB 11; Length 489;

Query Match

```
APPLICATION NUMBER: EPO 94810439.3
          FILING DATE: 25-Jul-94
      ATTORNEY/AGENT INFORMATION:
          NAME: Pfeiffer, Hesna J.
          REGISTRATION NUMBER: 22640
          REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: (908) 522-6940
          TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 1:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 339 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
      MOLECULE TYPE: cDNA to mRNA
      HYPOTHETICAL: NO
       IMMEDIATE SOURCE:
          CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
      FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "human TGF-beta1"
       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1
 Query Match
                    85.0%; Score 308.6; DB 10; Length 339;
                  94.4%; Pred. No. 4.9e-83;
 Best Local Similarity
 Matches 320; Conservative
                         0; Mismatches
                                     19; Indels
                                                 0; Gaps
                                                           0;
        Qy
           Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Dh
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
       121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
       205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGGCGC 264
Qу
           181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCGCGCA40
Db
Qу
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
           Db
       241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
QУ
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Dh
       301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
```

```
; Sequence 1, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
 TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
 CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
  LENGTH: 1821
  TYPE: DNA
  ORGANISM: Human
  FEATURE:
  NAME/KEY: 5'UTR
  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
  OTHER INFORMATION:
  NAME/KEY: sig peptide
  LOCATION: (512)..(598)
  OTHER INFORMATION:
  NAME/KEY: 3'UTR
  LOCATION: (1685) .. (1821)
  OTHER INFORMATION:
US-10-087-268-1
 Query Match
                  85.0%; Score 308.6; DB 14; Length 1821;
 Best Local Similarity 94.4%; Pred. No. 6.9e-83;
 Matches 320; Conservative
                       0; Mismatches 19; Indels
                                               0; Gaps
                                                        0;
        25 GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGGCGGCAGCTC 84
Qy
          Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          1406 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1465
Db
Qу
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
          Db
      1466 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1525
Qу
       Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
      1586 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1645
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
```

```
RESULT 4
US-10-087-268-4
; Sequence 4, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
 TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
 CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
  LENGTH: 1821
  TYPE: DNA
  ORGANISM: Human
  FEATURE:
  NAME/KEY: 5'UTR
  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
  OTHER INFORMATION:
  NAME/KEY: sig peptide
  LOCATION: (51\overline{2})...(598)
  OTHER INFORMATION:
  NAME/KEY: 3'UTR
  LOCATION: (1685)..(1821)
  OTHER INFORMATION:
US-10-087-268-4
 Query Match
                  85.0%; Score 308.6; DB 14; Length 1821;
 Best Local Similarity 94.4%; Pred. No. 6.9e-83;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                              0; Gaps
                                                       0:
       Qу
          Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          1406 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1465
Dh
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          1466 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1525
Db
       Qу
          Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
```

```
Db
       1586 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1645
Qу
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
            Db
       1646 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1684
RESULT 5
US-10-037-270-220
; Sequence 220, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
; APPLICANT: Zhanq, Jie
; APPLICANT: Ren, Feiyan
  APPLICANT: Chen, Rui-hong
  APPLICANT: Zhao, Oing A.
 APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
 APPLICANT: Wang, Dunrui
  APPLICANT: Wang, Zhiwei
 APPLICANT: Tillinghast, John
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
  CURRENT APPLICATION NUMBER: US/10/037,270
  CURRENT FILING DATE: 2002-01-04
  PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
  NUMBER OF SEO ID NOS: 1104
  SOFTWARE: pt FL genes Version 1.0
; SEO ID NO 220
  LENGTH: 2742
   TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
   LOCATION: (842)..(2014)
US-10-037-270-220
 Query Match
                      85.0%; Score 308.6; DB 14; Length 2742;
 Best Local Similarity
                      94.4%; Pred. No. 7.5e-83;
 Matches 320; Conservative
                           0; Mismatches
                                          19; Indels
                                                       0; Gaps
                                                                  0;
Qу
         25 GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGGCGGCAGCTC 84
            Db
```

```
Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
       1736 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1795
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
       1796 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1855
Qу
       205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGGGGGCGCGTGCTGCGTGCCG 264
           Db
       1856 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCGTGCCG 1915
Qу
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
           Db
      1916 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1975
Qу
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
      1976 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
RESULT 6
US-09-948-002-28
; Sequence 28, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
 TITLE OF INVENTION: FACTOR BETA EXPRESSION
 FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
SEO ID NO 28
  LENGTH: 2745
  TYPE: DNA
  ORGANISM: Homo sapiens
   FEATURE:
  NAME/KEY: CDS
  LOCATION: (842)...(2017)
US-09-948-002-28
 Query Match
                    85.0%; Score 308.6; DB 11; Length 2745;
 Best Local Similarity 94.4%; Pred. No. 7.5e-83;
 Matches 320; Conservative
                        0; Mismatches
                                      19; Indels
                                                 0; Gaps
                                                           0;
Qу
        Db
Оy
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
```

```
Db
      1739 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1798
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
      1799 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1858
       Qу
          Db
      1859 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCGTGCTGCCG 1918
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
      1919 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1978
Qу
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
          Db
      1979 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2017
RESULT 7
US-09-948-002-27
; Sequence 27, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
 APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                            EXPRESSION
 FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
 NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 27
  LENGTH: 1585
  TYPE: DNA
  ORGANISM: Rattus norvegicus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (413)...(1585)
US-09-948-002-27
 Query Match
                   79.3%; Score 287.8; DB 11; Length 1585;
 Best Local Similarity 90.6%; Pred. No. 1.2e-76;
 Matches 307; Conservative 0; Mismatches 32; Indels
                                                0; Gaps
                                                         0;
Qу
        Db
      1247 GCCCTGGATACCAACTACTGCTTCAGCTCCACAGAGAAGAACTGCTGTGTACGGCAGCTG 1306
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          Db
      1307 TACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1366
```

```
Оv
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
           Db
       1367 GCCAACTTCTGTCTGGGGCCCTGCCCCTACATTTGGAGCCTGGACACAGTACAGCAAG 1426
Qу
       1427 GTCCTTGCCCTCTACAACCAACACACCCGGGTGCTTCCGCATCACCGTGCTGCGTGCCG 1486
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           1487 CAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGCAAGCCCAAGGTGGAGCAG 1546
Db
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       1547 TTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1585
RESULT 8
US-09-948-002-1
; Sequence 1, Application US/09948002
: Publication No. US20030050265A1
; GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
 APPLICANT: Susan F. Murray
 TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                            EXPRESSION
 FILE REFERENCE: ISPH-0607
 CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 09/661,753
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 1
  LENGTH: 2094
   TYPE: DNA
  ORGANISM: Mus musculus
  FEATURE:
   NAME/KEY: CDS
  LOCATION: (868)...(2040)
US-09-948-002-1
                   79.3%; Score 287.8; DB 11; Length 2094;
 Query Match
 Best Local Similarity 90.6%; Pred. No. 1.3e-76;
 Matches 307; Conservative 0; Mismatches 32; Indels
                                                 0; Gaps
                                                           0;
Qу
        1702 GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAACTGCTGTGTGCGGCAGCTG 1761
Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qy
          Db
      1762 TACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1821
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
```

```
Db
       1822 GCCAACTTCTGTCTGGGACCCTGCCCCTATATTTGGAGCCTGGACACACAGTACAGCAAG 1881
        Qу
            1882 GTCCTTGCCCTCTACAACCAACACACCCGGGCGCTTCGGCGTCACCGTGCTGCCGCG 1941
Dh
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
            1942 CAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGCAAGCCCAAGGTGGAGCAG 2001
Db
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
             2002 TTGTCCAACATGATTGTGCGCTCCTGCAAGTGCAGCTGA 2040
Dh
RESULT 9
US-09-813-271B-7
; Sequence 7, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
       APPLICANT:
                 (A) Nico Cerletti
       TITLE OF INVENTION: New process for the production of
                        biologically active protein
       NUMBER OF SEQUENCES: 13
       CORRESPONDENCE ADDRESS:
           ADDRESSEE: No. US20020115834Alartis Patent Department
           STREET: 564 Morris Avenue
           CITY: Summit
           STATE: New Jersey
           COUNTRY: USA
           ZIP: 07901
       COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/813,271B
           FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: PCT/EP95/02719
           FILING DATE: 12-Jul-95
           APPLICATION NUMBER: EPO 94810439.3
           FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
           NAME: Pfeiffer, Hesna J. .
           REGISTRATION NUMBER: 22640
           REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
           TELEPHONE: (908) 522-6940
           TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 7:
       SEQUENCE CHARACTERISTICS:
           LENGTH: 336 base pairs
           TYPE: nucleic acid
```

```
STRANDEDNESS: double
          TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
          DESCRIPTION: /desc = "recombinant hybrid DNA of
      IMMEDIATE SOURCE:
          CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
      FEATURE:
          NAME/KEY: mat_peptide
          LOCATION: 1..132
          OTHER INFORMATION: /product= "N-terminal 44 amino
          acids of human TGF-betal"
      FEATURE:
          NAME/KEY: mat_peptide
          LOCATION: 133..336
          OTHER INFORMATION: /product= "C-terminal 68 amino
          acids of human TGF-beta3"
      FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "hybrid TGF-beta named
          TGF-beta1-3"
      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-813-271B-7
 Query Match
                   62.6%; Score 227.2; DB 10; Length 336;
 Best Local Similarity 79.8%; Pred. No. 1.4e-58;
 Matches 268; Conservative
                       0; Mismatches
                                     68; Indels
                                                 0; Gaps
                                                          0;
Qу
        Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          Db
        61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           111111
Db
       121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACCAACCCACAGCACG 180
       Qу
           ]| ||| || || ||||||
                         Db
       181 GTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCC 240
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
       241 CAGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 300
ŨУ
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGC 360
          Db
       301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
RESULT 10
US-09-906-158-10
; Sequence 10, Application US/09906158
; Publication No. US20030078217A1
```

```
; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
  FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 10
   LENGTH: 2879
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (611)...(1843)
US-09-906-158-10
                     58.2%; Score 211.2; DB 11; Length 2879;
 Query Match
 Best Local Similarity 75.9%; Pred. No. 1.4e-53;
 Matches 261; Conservative
                         0; Mismatches
                                       83; Indels
                                                    0; Gaps
                                                              0;
Оy
        Dh
       1500 AGAGGGCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTTACGCC 1559
        80 AGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCT 139
Qу
             1560 CCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTT 1619
Dh
Qу
        140 ACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACA 199
           Db
       1620 ACTATGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGCGCAGACACACCCATA 1679
Qу
        200 GCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCG 259
           Db
       1680 GCACGGTGCTTGGACTATACAACACCCTGAACCCAGAGGCGTCTGCCTCGCCATGCTGCG 1739
        260 TGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGG 319
Qу
           1740 TCCCCCAGGACCTGGAGCCCTGACCATCTTGTACTATGTGGGCAGAACCCCCAAGGTGG 1799
Db
Qу
        320 AGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Dh
       1800 AGCAGCTGTCCAACATGGTGGTGAAGTCGTGTAAGTGCAGCTGA 1843
RESULT 11
US-09-957-458B-9
; Sequence 9, Application US/09957458B
; Publication No. US20030166271A1
; GENERAL INFORMATION:
 APPLICANT: Chen, Una
  TITLE OF INVENTION: Method for growing stem cells
 FILE REFERENCE: P66567US0
; CURRENT APPLICATION NUMBER: US/09/957,458B
  CURRENT FILING DATE: 2001-09-21
```

```
PRIOR APPLICATION NUMBER: PCT/EP00/08247
  PRIOR FILING DATE: 2000-08-24
  PRIOR APPLICATION NUMBER: EP 99116533
  PRIOR FILING DATE: 1999-08-24
  NUMBER OF SEQ ID NOS: 10
  SOFTWARE: PatentIn version 3.2
; SEO ID NO 9
   LENGTH: 4382
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Vector for transforming supporting cell with a foreign to
express
   OTHER INFORMATION: a gene product of interest
US-09-957-458B-9
 Query Match
                     58.2%; Score 211.2; DB 12; Length 4382;
 Best Local Similarity
                     75.9%; Pred. No. 1.5e-53;
 Matches 261; Conservative
                          0; Mismatches
                                       83; Indels
                                                    0; Gaps
                                                              0:
QУ
         Db
       1353 AGAGGGCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTTACGCC 1412
Qу
         80 AGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCT 139
             Dh
       1413 CCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTT 1472
        140 ACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACA 199
Qу
           Db
       1473 ACTATGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGCGCAGACACACCCATA 1532
        200 GCAAGGTCCTGGCTCTGTACAACCAGCACACCCGGGCGCGTCGGCGGCGCGTGCTGCG 259
Qу
           1533 GCACGGTGCTTGGACTATACAACACCCTGAACCCAGAGGCGTCTGCCTCGCCATGCTGCG 1592
Db
        260 TGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGG 319
Qу
           1593 TCCCCCAGGACCTGGACCCTGACCATCTTGTACTATGTGGGCAGAACCCCCAAGGTGG 1652
Db
        320 AGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       1653 AGCAGCTGTCCAACATGGTGGTGAAGTCGTGTAAGTGCAGCTGA 1696
RESULT 12
US-09-906-158-3
; Sequence 3, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
 FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
```

```
NUMBER OF SEQ ID NOS: 168
 SEO ID NO 3
   LENGTH: 2574
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (254)...(1492)
US-09-906-158-3
 Query Match
                     58.0%; Score 210.4; DB 11; Length 2574;
 Best Local Similarity 76.2%; Pred. No. 2.4e-53;
 Matches 259; Conservative
                         0; Mismatches 81; Indels
                                                    0; Gaps
                                                              0;
         Qу
           Db
       1153 GGCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCT 1212
         84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
Qу
           Db
       1213 CTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTA 1272
        144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
Qу
           \{\{\}\}\}
Db
       1273 TGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACAACCCACAGCAC 1332
        204 GGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCCC 263
Qу
           Db
       1333 GGTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCC 1392
Qу
        264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
            Db
       1393 CCAGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCA 1452
QУ
        324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
       1453 GCTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 1492
RESULT 13
US-10-028-158-20
; Sequence 20, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
 APPLICANT: Caniggia, Isabella
 APPLICANT: Post, Martin
 APPLICANT: Lye, Stephen
  TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
  TITLE OF INVENTION: TROPHOBLAST
  FILE REFERENCE: 11757.38USWO
  CURRENT APPLICATION NUMBER: US/10/028,158
  CURRENT FILING DATE: 2001-12-20
  PRIOR APPLICATION NUMBER: US/09/380,662
 PRIOR FILING DATE: 1999-12-21
  PRIOR APPLICATION NUMBER: PCT/CA98/00180
  PRIOR FILING DATE: 1998-03-05
  PRIOR APPLICATION NUMBER: US 60/039,919
```

```
NUMBER OF SEQ ID NOS: 24
  SOFTWARE: PatentIn version 3.0
 SEO ID NO 20
  LENGTH: 2574
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (254)..(1492)
US-10-028-158-20
 Query Match
                    58.0%; Score 210.4; DB 13; Length 2574;
 Best Local Similarity 76.2%; Pred. No. 2.4e-53;
 Matches 259; Conservative 0; Mismatches 81; Indels
                                                  0; Gaps
                                                             0;
QУ
        Db
       1153 GGCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCT 1212
        84 CTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCA 143
Qу
           1213 CTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTA 1272
Db
Qу
       144 TGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAA 203
           Db
       1273 TGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACACCCACAGCAC 1332
        204 GGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCC 263
Qу
           1333 GGTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCC 1392
Db
       264 GCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 323
Qу
            Db
       1393 CCAGGACCTGGACCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCA 1452
       324 GCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       1453 GCTCTCCAACATGTGGTGAAGTCTTGTAAATGTAGCTGA 1492
RESULT 14
US-09-813-271B-5
; Sequence 5, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
      APPLICANT:
                (A) Nico Cerletti
       TITLE OF INVENTION: New process for the production of
                      biologically active protein
      NUMBER OF SEQUENCES: 13
      CORRESPONDENCE ADDRESS:
          ADDRESSEE: No. US20020115834Alartis Patent Department
           STREET: 564 Morris Avenue
          CITY: Summit
           STATE: New Jersey
          COUNTRY: USA
```

PRIOR FILING DATE: 1997-03-07

```
COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/813,271B
           FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: PCT/EP95/02719
           FILING DATE: 12-Jul-95
           APPLICATION NUMBER: EPO 94810439.3
           FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
           NAME: Pfeiffer, Hesna J. .
           REGISTRATION NUMBER: 22640
           REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
           TELEPHONE: (908) 522-6940
           TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 5:
       SEQUENCE CHARACTERISTICS:
           LENGTH: 339 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
       MOLECULE TYPE: cDNA to mRNA
       IMMEDIATE SOURCE:
           CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)
       FEATURE:
           NAME/KEY: CDS
           LOCATION: 1..336
           OTHER INFORMATION: /product= "human TGF-beta3"
       SEQUENCE DESCRIPTION: SEO ID NO: 5:
US-09-813-271B-5
 Query Match
                     57.7%; Score 209.4; DB 10; Length 339;
 Best Local Similarity 76.1%; Pred. No. 3.2e-53;
 Matches 258; Conservative 0; Mismatches 81; Indels
         Qу
           Db
         1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCTC 60
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           Db
         61 TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Dh
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCC 264
QУ
           Db
        181 GTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCCGCCC 240
```

ZIP: 07901

```
Qу
         265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
             Db
         241 CAGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 300
         325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
             Db
         301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 339
RESULT 15
US-09-813-271B-11
; Sequence 11, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
        APPLICANT:
                   (A) Nico Cerletti
        TITLE OF INVENTION: New process for the production of
                           biologically active protein
        NUMBER OF SEQUENCES: 13
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: No. US20020115834Alartis Patent Department
             STREET: 564 Morris Avenue
             CITY: Summit
             STATE: New Jersey
             COUNTRY: USA
             ZIP: 07901
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/813,271B
             FILING DATE: 20-Mar-2001
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: PCT/EP95/02719
             FILING DATE: 12-Jul-95
             APPLICATION NUMBER: EPO 94810439.3
             FILING DATE: 25-Jul-94
        ATTORNEY/AGENT INFORMATION:
             NAME: Pfeiffer, Hesna J. .
             REGISTRATION NUMBER: 22640
             REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (908) 522-6940
             TELEFAX: (908) 522-6955
  INFORMATION FOR SEQ ID NO: 11:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 336 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: other nucleic acid
             DESCRIPTION: /desc = "recombinant hybrid DNA
        IMMEDIATE SOURCE:
             CLONE: E. coli LC137/pPLMu.TGF-beta3(44/45)beta2
        FEATURE:
```

```
NAME/KEY: mat peptide
          LOCATION: 1..132
          OTHER INFORMATION: /product = "N-terminal 44 amino
          acids of human TGF-beta3"
      FEATURE:
          NAME/KEY: mat_peptide
          LOCATION: 133..336
          OTHER INFORMATION: /product= "C-terminal 68 amino
          acids of human TGF-beta2"
      FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "hybrid TGF-beta3-2"
      SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-813-271B-11
 Ouery Match
                   50.2%; Score 182.4; DB 10; Length 336;
 Best Local Similarity 71.4%; Pred. No. 4.1e-45;
 Matches 240; Conservative
                       0; Mismatches
                                     96; Indels
                                                          0:
        Qу
          Db
         1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCTC 60
Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
          Db
        61 TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
       121 GCCAACTTCTGTGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCAGCAGCAGG 180
       Qу
          181 GTCCTGAGCTTATATAATACCATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCC 240
Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
       241 CAAGATTTAGAACCTCTAACCATTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGC 360
Qу
          Db
       301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336
Search completed: October 28, 2003, 09:04:08
Job time : 109.037 secs
                     GenCore version 5.1.6
             Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 900.804 Seconds (without alignments) 9794.056 Million cell updates/sec

```
Sequence:
               1 gactacaaggatgacgacga.....gttcctgcaagtgcagctga 363
Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0
Searched:
               22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries
Database :
                EST: *
               1: em_estba:*
               2: em_esthum:*
               3: em estin:*
               4: em estmu:*
               5: em estov:*
               6: em_estpl:*
               7: em estro:*
               8: em_htc:*
               9: gb est1:*
               10: gb est2:*
               11: qb htc:*
               12: gb est3:*
               13: gb est4:*
               14: gb_est5:*
               15: em_estfun:*
               16: em_estom:*
               17: em_gss hum:*
               18: em_gss_inv:*
               19: em gss pln:*
               20: em_gss_vrt:*
               21: em_gss_fun:*
               22: em_gss_mam:*
               23: em_gss_mus:*
               24: em gss pro:*
               25: em gss rod:*
               26: em_gss_phg:*
               27: em_gss_vrl:*
               28: gb gssl:*
               29:
                    gb gss2:*
```

US-10-017-372E-10

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a

왕

Title:

Perfect score: 363

	No.	Score	Match	Length	DB	ID	Description AI951831 wx38h08.x
c	1	310.2	85.5	598	9	AI951831	AI951831 wx38b08.x
	2	308.6	85.0	396	12	BI868266	
	3	308.6	85.0	400	12	BI820759	BI820759 603034355
	4	308.6	85.0	461	12	BM740537	BM740537 K-EST0011
	5	308.6	85.0	505	10	AW958056	AW958056 EST370126
	6	308.6	85.0	536	13	BQ222205	BQ222205 AGENCOURT
С	7	308.6	85.0	538	12	BM670402	BM670402 UI-E-DW1-
	8	308.6	85.0	540	12	BI834732	BI834732 603090326
С	9	308.6	85.0	593	12	BQ003136	BQ003136 UI-H-EI1-
_	10	308.6	85.0	599	12	BI905963	BI905963 603062849
C	11	308.6	85.0	600	10	BF726995	BF726995 by15c03.y
C	12	308.6	85.0	616	12	BM674987	BM674987 UI-E-EJO-
C	13 14	308.6 308.6	85.0 85.0	625 649	14	CA426732	CA426732 UI-H-FE1-
C	15	308.6	85.0	654	14 12	CA423539 BM681750	CA423539 UI-H-FE1-
C	16	308.6	85.0	662	13	BQ576225	BM681750 UI-E-EJ0- BQ576225 UI-H-EZ1-
C	17	308.6	85.0	674	14	CA503085	CA503085 UI-CF-FN0
С	18	308.6	85.0	676	13	BU737545	BU737545 UI-E-DW1-
C	19	308.6	85.0	677	14	CA432581	CA432581 UI-H-FL1-
C	20	308.6	85.0	678	12	BQ021537	BQ021537 UI-H-DH1-
С	21	308.6	85.0	690	13	BU625377	BU625377 UI-H-FG1-
C	22	308.6	85.0	695	14	CA425775	CA425775 UI-H-FE1-
C	23	308.6	85.0	697	13	BU633535	BU633535 UI-H-FL1-
С	24	308.6	85.0	697	14	CA426391	CA426391 UI-H-FE1-
C	25	308.6	85.0	700	13	BU633922	BU633922 UI-H-FL1-
C	26	308.6	85.0	722	13	BU632686	BU632686 UI-H-FE1-
C	27	308.6	85.0	757	14	CA309731	CA309731 UI-H-FT1-
С	28	308.6	85.0	888	13	BX434425	BX434425 BX434425
С	29	308.6	85.0	928	13	BX412434	BX412434 BX412434
С	30	308.6	85.0	956	12	BI084718	BI084718 602869722
	31	308.6	85.0	1181	12	BM805377	BM805377 AGENCOURT
	32 33	307.6 307.6	84.7	427	12	BM738551	BM738551 K-EST0006
	34	307.6	84.7 84.7	451 1093	12 12	BM717493 BQ054305	BM717493 UI-E-EJ0- BQ054305 AGENCOURT
С	35	307.6	84.7	1201	13	BX355682	BX355682 BX355682
C	36	307.4	84.7	660	12	BM251237	BM251237 BOTL01000
С	37	307	84.6	583	13	BU625902	BU625902 UI-H-FG1-
C	38		84.6			BQ016027	BQ016027 UI-H-DT1-
C	39	307	84.6	655	13	BU624264	BU624264 UI-H-FG1-
С	40	307	84.6	661	12	BQ021516	BQ021516 UI-H-DH1-
С	41	307	84.6	720	14	CA416525	CA416525 UI-H-FE0-
С	42	307	84.6	727	9	AI131171	AI131171 gc15c11.x
	43	307	84.6	1111	12	BI833863	BI833863 603088633
C	44	306.6	84.5	535	14	CA431985	CA431985 UI-H-FL1-
С	45	305.8	84.2	568	10	BE464068	BE464068 hx84h02.x

ALIGNMENTS

RESULT 1 AI951831/c

LOCUS AI951831 598 bp mRNA linear EST 06-SEP-1999
DEFINITION wx38b08.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545911 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1

```
PRECURSOR (HUMAN); contains PTR7.t3 MER22 repetitive element ;, mRNA
           sequence.
ACCESSION
           AI951831
           AI951831.1 GI:5744141
VERSION
KEYWORDS
           EST.
SOURCE
           Homo sapiens (human)
  ORGANISM
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 598)
 AUTHORS
           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  TITLE
           Tumor Gene Index
  JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
           Emmert-Buck, M.D., cDNA Library Preparation: Life Technologies,
           Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.
           Consortium DNA Sequencing by: Washington University Genome
           Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Seq primer: -40UP from Gibco
           High quality sequence stop: 425.
FEATURES
                   Location/Qualifiers
                   1. .598
    source
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db xref="taxon:9606"
                   /clone="IMAGE: 2545911"
                   /tissue type="four pooled pituitary adenomas"
                   /lab host="DH10B"
                   /clone lib="NCI CGAP Pit1"
                   /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
                   Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                   Library constructed by Life Technologies."
BASE COUNT
               95 a
                       173 c
                               222 q
                                       107 t
                                                  1 others
ORIGIN
  Query Match
                        85.5%; Score 310.2; DB 9; Length 598;
  Best Local Similarity 93.4%; Pred. No. 1.8e-66;
 Matches 324; Conservative 0; Mismatches
                                              23; Indels
                                                            0; Gaps
                                                                        0;
          17 ACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGC 76
Qу
                484 ACCGCGAAGCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGC 425
Dh
          77 GGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGG 136
Qу
             Db
         424 GGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGG 365
         137 GCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGT 196
QУ
             Db
         364 GCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGT 305
```

```
Qу
         197 ACAGCAAGGTCCTGGCTCTGTACAACCAGCACACCCGGGCGCGTCGGCGGCGCCGTGCT 256
             Db
         304 ACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCT 245
         257 GCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGG 316
Qу
             Db
         244 GCGTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGG 185
         317 TGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
             184 TGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 138
Db
RESULT 2
BI868266
LOCUS
           BI868266
                                  396 bp
                                           mRNA
                                                   linear
                                                           EST 11-OCT-2001
DEFINITION 603392221F1 NIH MGC 90 Homo sapiens cDNA clone IMAGE:5402212 5',
           mRNA sequence.
           BI868266
ACCESSION
           BI868266.1 GI:16041939
VERSION
KEYWORDS
           EST.
SOURCE
           Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 396)
           NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
           National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM12025 row: j column: 05
           High quality sequence stop: 383.
FEATURES
                   Location/Qualifiers
    source
                   1. .396
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db xref="taxon:9606"
                   /clone="IMAGE:5402212"
                   /tissue_type="adenocarcinoma, cell line"
                   /lab_host="DH10B (phage-resistant)"
                   /clone_lib="NIH_MGC 90"
                   /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                   Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
                   Average insert size 1.7 kb. Library enriched for
                   full-length clones and constructed by Life Technologies.
                   Note: this is a NIH MGC Library."
BASE COUNT
                       135 c
               75 a
                               121 g
                                        65 t
ORIGIN
```

```
Query Match
                    85.0%; Score 308.6; DB 12; Length 396;
 Best Local Similarity 94.4%; Pred. No. 3.8e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                    0; Gaps
                                                              0;
Qу
        Db
        Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
        101 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 160
Qу
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
            Db
        161 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 220
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCG 264
Qу
           221 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCG 280
Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
           281 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 340
Db
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           341 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 379
Db
RESULT 3
BI820759
LOCUS
         BI820759
                             400 bp
                                     mRNA
                                            linear
                                                   EST 04-OCT-2001
DEFINITION 603034355F1 NIH MGC 115 Homo sapiens cDNA clone IMAGE:5175732 5',
         mRNA sequence.
ACCESSION
         BI820759
         BI820759.1 GI:15932309
VERSION
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 400)
         NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
         National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11437 row: m column: 13
         High quality sequence stop: 364.
FEATURES
                Location/Qualifiers
```

```
1. .400
    source
                /organism="Homo sapiens"
                /mol type="mRNA"
                /db xref="taxon:9606"
                /clone="IMAGE:5175732"
                /lab host="DH10B"
                /clone lib="NIH MGC 115"
                /note="Organ: pooled brain, lung, testis; Vector:
                pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                source anonymous pool of 6 male brains, age range 23-27; 1
                male lung, age 27; and 1 male testis, age 69. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.8 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
                Gruber (Invitrogen). Research Genetics tracking code
                021. Note: this is a NIH MGC Library."
BASE COUNT
             73 a
                   131 c
                           131 g
                                  65 t
ORIGIN
                    85.0%; Score 308.6; DB 12; Length 400;
 Query Match
 Best Local Similarity
                    94.4%;
                          Pred. No. 3.8e-66;
 Matches 320; Conservative
                          0; Mismatches
                                       19; Indels
                                                   0; Gaps
                                                             0;
Qy
        Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           Db
        80 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 139
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           140 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 199
Dh
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCGGCGCCGTGCTGCCG 264
Qу
           200 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCCGTGCTGCGTGCCG 259
Db
Qу
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
           Db
       260 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 319
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Db
       320 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 358
RESULT 4
BM740537
LOCUS
         BM740537
                             461 bp
                                     mRNA
                                           linear
                                                  EST 01-MAR-2002
DEFINITION
         K-EST0011722 S1SNU5 Homo sapiens cDNA clone S1SNU5-5-B09 5', mRNA
         sequence.
         BM740537
ACCESSION
```

VERSION

KEYWORDS

EST.

BM740537.1 GI:19061866

```
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 461)
           Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 AUTHORS
           Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
           Kim, Y.S.
 TITLE
           21C Frontier Korean EST Project 2001
 JOURNAL
           Unpublished
COMMENT
           Contact: Kim YS
           Genome Research Center
           Korea Research Institute of Bioscience & Biotechnology
           52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
           Tel: +82-42-860-4470
           Fax: +82-42-860-4409
           Email: yongsung@mail.kribb.re.kr
           Plate: 5 row: B column: 09
           High quality sequence stop: 461.
FEATURES
                   Location/Qualifiers
                   1. .461
    source
                   /organism="Homo sapiens"
                   /mol type="mRNA"
                   /db xref="taxon:9606"
                   /clone="S1SNU5-5-B09"
                   /sex="F"
                   /tissue type="Ascites"
                   /cell_type="Lymphoblast-like"
                   /cell_line="SNU-5"
                   /lab host="Top10F'"
                   /clone lib="S1SNU5"
                   /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
                   Site 2: NotI; The poly (A) + RNA was dephosphorylated with
                   bacterial alkaline phosphatase (BAP) and then decapped
                   with tabacco acid pyrophosphatase (TAP). The decapped
                   intact mRNA was ligated with DNA-RNA linker including EcoR
                   I site by treatment of T4 RNA ligase and the first strand
                   cDNA was synthesized from oligo dT-selected mRNA by
                   priming with dT-tailed vector. The dT-tailed vector was
                   adjusted to have about 60nt. The cDNA vector was
                   circularized with E. coli DNA ligase after digestion of
                   EcoRI which site is also included in vector. An RNA strand
                   converted to a DNA strand by Okayama-Berg method. The
                   obtained cDNA vectors were used for transformation of
                   competent cells E. coli Top10F' by electroporation method.
                   The cDNA libraries constructed by this method are
                   full-length enriched cDNA library."
               86 a
                       161 c
BASE COUNT
                              133 g
                                        81 t
ORIGIN
 Ouery Match
                        85.0%; Score 308.6; DB 12; Length 461;
 Best Local Similarity
                        94.4%; Pred. No. 4e-66;
 Matches 320; Conservative
                              0; Mismatches
                                             19; Indels
                                                            0: Gaps
                                                                       0;
          QУ
             Db
```

SOURCE

Homo sapiens (human)

```
85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
            Db
        179 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 238
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
            Db
        239 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 298
        Qу
            Db
        299 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGCGCCGTGCTGCCG 358
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
            Db
        359 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 418
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
            Db
        419 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 457
RESULT 5
AW958056
LOCUS
          AW958056
                               505 bp
                                       mRNA
                                              linear
                                                      EST 01-JUN-2000
DEFINITION EST370126 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION
          AW958056
          AW958056.1 GI:8147739
VERSION
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 505)
 AUTHORS
          Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
          , I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
          Quackenbush, J.
 TITLE
          Assessment of gene expression patterns in a model of colon tumor
          metastasis using a 19,200 element cDNA microarray
 JOURNAL
          Unpublished
COMMENT
          Contact: John Quackenbush
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 3528
          Fax: 301 838 0208
          Email: johnq@tigr.org
          Plate: 115
          Seq primer: Reverse.
FEATURES
                 Location/Qualifiers
    source
                 1. .505
                 /organism="Homo sapiens"
                 /mol type="mRNA"
                 /db xref="taxon:9606"
                 /clone lib="MAGE resequences, MAGE"
                 /note="Vector: pBluescriptSKm"
BASE COUNT
             115 a 137 c
                            106 g
                                  144 t
                                             3 others
ORIGIN
```

```
Query Match
                     85.0%; Score 308.6; DB 10; Length 505;
 Best Local Similarity
                    94.4%; Pred. No. 4.1e-66;
                         0; Mismatches
 Matches 320; Conservative
                                       19; Indels
                                                    0; Gaps
                                                              0;
Qу
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           Db
         69 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 128
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
        129 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 188
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCGTGCCG 264
Qу
           Db
        189 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCGCGTGCTGCCG 248
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
        249 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 308
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
QУ
           309 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 347
Dh
RESULT 6
BQ222205
LOCUS
         BQ222205
                             536 bp
                                     mRNA
                                            linear
                                                   EST 02-MAY-2002
DEFINITION
         AGENCOURT 7258595 NIH MGC 71 Homo sapiens cDNA clone IMAGE:5786680
         5', mRNA sequence.
ACCESSION
         B0222205
         BQ222205.1 GI:20403594
VERSION
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM
         Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 536)
 AUTHORS
         NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
         National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM12875 row: m column: 17
         High quality sequence stop: 535.
```

```
FEATURES
               Location/Qualifiers
   source
               1. .536
               /organism="Homo sapiens"
               /mol type="mRNA"
               /db xref="taxon:9606"
               /clone="IMAGE:5786680"
               /tissue type="leiomyosarcoma"
               /lab host="DH10B (phage-resistant)"
               /clone lib="NIH MGC 71"
               /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 2.1 kb. "
BASE COUNT
           113 a
                  193 c
                        150 g
                               77 t
                                      3 others
ORIGIN
 Ouery Match
                  85.0%; Score 308.6; DB 13; Length 536;
 Best Local Similarity
                  94.4%; Pred. No. 4.2e-66;
 Matches 320; Conservative
                      0; Mismatches 19; Indels
                                              0; Gaps
                                                       0;
       Qу
          Db
       85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
          96 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 155
Db
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
          Db
       156 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 215
       Qу
          Db
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
          Db
       276 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 335
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
          Dh
       336 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 374
RESULT 7
BM670402/c
LOCUS
        BM670402
                          538 bp
                                 mRNA
                                             EST 27-FEB-2002
                                       linear
DEFINITION
        UI-E-DW1-ahc-1-03-0-UI.sl UI-E-DW1 Homo sapiens cDNA clone
        UI-E-DW1-ahc-1-03-0-UI 3', mRNA sequence.
ACCESSION
        BM670402
VERSION
        BM670402.1 GI:18980299
KEYWORDS
        EST.
SOURCE
        Homo sapiens (human)
 ORGANISM
        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE

1 (bases 1 to 538)

```
AUTHORS
            Bonaldo, M.F., Lennon, G. and Soares, M.B.
            Normalization and subtraction: two approaches to facilitate gene
  TITLE
            discovery
            Genome Res. 6 (9), 791-806 (1996)
  JOURNAL
            97044477
  MEDLINE
   PUBMED
            8889548
COMMENT
            Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
             The following repetitive elements were found in this cDNA
            sequence: 97-152, >GC rich#Low complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES
                     Location/Qualifiers
                     1. .538
     source
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="UI-E-DW1-ahc-1-03-0-UI"
                     /tissue_type="lens"
                     /dev stage="adult"
                     /lab host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-DW1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-E-DW1 is a normalized CDNA library containing the
                     following tissue(s): lens. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CGATTAGCGA. This library
                     was created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI).
                     TAG LIB=UI-E-DW1
                     TAG TISSUE=human lens
                     TAG_SEQ=CGATTAGCGA"
BASE COUNT
                 78 a
                         153 c
                                 195 g
                                           112 t
ORIGIN
  Query Match
                          85.0%; Score 308.6; DB 12; Length 538;
  Best Local Similarity 94.4%; Pred. No. 4.2e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                               0; Gaps
                                                                             0:
```

```
QУ
           Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
           Db
        434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
Db
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGGCGCGCGTGCTGCGTGCCG 264
Qу
           314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCG 255
Db
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
Db
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
QУ
           194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
Dh
RESULT 8
BI834732
LOCUS
         BI834732
                             540 bp
                                     mRNA
                                           linear
                                                   EST 04-OCT-2001
DEFINITION 603090326F1 NIH_MGC 120 Homo sapiens cDNA clone IMAGE:5229246 5',
         mRNA sequence.
ACCESSION
         BI834732
         BI834732.1 GI:15946269
VERSION
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM
         Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            (bases 1 to 540)
REFERENCE
 AUTHORS
         NIH-MGC http://mgc.nci.nih.gov/.
         National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11577 row: c column: 07
         High quality sequence stop: 535.
FEATURES
                Location/Qualifiers
                1. .540
   source
                /organism="Homo sapiens"
                /mol type="mRNA"
```

```
/db xref="taxon:9606"
                 /clone="IMAGE:5229246"
                 /lab host="DH10B"
                 /clone lib="NIH MGC 120"
                 /note="Organ: pooled pancreas and spleen; Vector:
                pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
                 source anonymous pool of spleen and pancreas from 28 yo
                male. Library is oligo-dT primed and directionally cloned
                 (EcoRV site is destroyed upon cloning). Average insert
                size 1.5 kb, insert size range 1-2.5 kb. Library is
                normalized and enriched for full-length clones and was
                constructed by C. Gruber (Invitrogen). Research Genetics
                tracking code 025. Note: this is a NIH MGC Library."
BASE COUNT
            104 a
                    188 c
                          154 g
                                   94 t
ORIGIN
                    85.0%; Score 308.6; DB 12; Length 540;
 Query Match
 Best Local Similarity
                    94.4%; Pred. No. 4.2e-66;
 Matches 320; Conservative 0; Mismatches
                                       19; Indels
                                                    0; Gaps
                                                             0;
Qу
        Db
        Oy
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           251 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 310
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
        311 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 370
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCG 264
Qу
           Db
        371 GTCCTGGCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCGCGTGCTGCGTGCCG 430
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
           431 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 490
Db
Qу
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
           Db
        491 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 529
RESULT 9
B0003136/c
LOCUS
         BQ003136
                             593 bp
                                     mRNA
                                           linear
                                                   EST 26-MAR-2002
DEFINITION
         UI-H-EI1-ayx-d-19-0-UI.sl NCI CGAP EI1 Homo sapiens cDNA clone
         IMAGE:5844834 3', mRNA sequence.
ACCESSION
         BQ003136
VERSION
         BQ003136.1 GI:19728036
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE
          1 (bases 1 to 593)
 AUTHORS
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
 JOURNAL
          Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Jose Mercuende
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           The following repetitive elements were found in this cDNA
           sequence: 97-152, >GC rich#Low complexity
           Seq primer: M13 FORWARD
           POLYA=Yes.
FEATURES
                   Location/Qualifiers
    source
                   1. .593
                   /organism="Homo sapiens"
                   /mol type="mRNA"
                   /db xref="taxon:9606"
                   /clone="IMAGE:5844834"
                   /tissue type="Chondrosarcoma"
                   /dev stage="Adult"
                   /lab host="DH10B (Life Technologies)"
                   /clone_lib="NCI_CGAP_EI1"
                   /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                   with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
                   NCI CGAP EI1 is a normalized cDNA library containing the
                   following tissue(s): Chondrosarcoma. The library was
                   constructed according to Bonaldo, Lennon and Soares,
                   Genome Research, 6:791-806, 1996. First strand cDNA
                   synthesis was primed with an oligo-dT primer containing a
                   Not I site. Double stranded cDNA was ligated to an EcoR I
                   adaptor, digested with Not I, and cloned directionally
                   into pT7T3-Pac vector. The oligonucleotide used to prime
                   the synthesis of first-strand cDNA contains a library tag
                   sequence that is located between the Not I site and the
                   (dT)18 tail. The sequence tag for this library is
                   ACACTTGCAC.
                   TAG LIB=UI-H-EI1
                   TAG TISSUE=chondrosarcoma
                   TAG SEQ=ACACTTGCAC"
BASE COUNT
               91 a
                      164 c
                              217 g
                                      121 t
ORIGIN
 Query Match
                       85.0%; Score 308.6; DB 12; Length 593;
 Best Local Similarity
                       94.4%; Pred. No. 4.4e-66;
                            0; Mismatches
 Matches 320; Conservative
                                            19; Indels
                                                          0; Gaps
                                                                     0;
QУ
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
```

```
Db
         434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
Qу
         145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
             Db
         374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
         205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGGGGGCGCCGTGCTGCCG 264
Qу
             Dh
         314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGCGCCGTGCTGCCG 255
         265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
             Dh
         254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
         325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
             Dh
         194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
RESULT 10
BI905963
LOCUS
                                                  linear
          BI905963
                                 599 bp
                                          mRNA
                                                          EST 16-OCT-2001
DEFINITION 603062849F1 NIH MGC 118 Homo sapiens cDNA clone IMAGE:5211925 5',
          mRNA sequence.
ACCESSION
          BI905963
VERSION
          BI905963.1 GI:16168598
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 599)
          NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11532 row: a column: 14
          High quality sequence stop: 567.
FEATURES
                   Location/Qualifiers
                   1. .599
    source
                   /organism="Homo sapiens"
                   /mol type="mRNA"
                   /db xref="taxon:9606"
                   /clone="IMAGE:5211925"
                   /tissue type="leukocyte"
                   /lab host="DH10B"
                   /clone lib="NIH MGC 118"
                   /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
                   (destroyed); RNA source leukocytes from anonymous pool of
```

non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."

BASE COUNT 112 a 201 c 181 g 105 t

ORIGIN

```
Query Match
              85.0%; Score 308.6; DB 12; Length 599;
 Best Local Similarity 94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                     0; Gaps
                                           0;
      Qу
        Db
     85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
        Db
     293 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 352
Qу
     145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
        Db
     353 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 412
     205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCCG 264
Qу
        Dh
     265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
        473 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 532
Db
     325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
```

```
RESULT 11
BF726995/c
```

Db

LOCUS BF726995 600 bp mRNA linear EST 05-JAN-2001 DEFINITION by15c03.y1 Human Lens cDNA (Un-normalized, unamplified): BY Homo sapiens cDNA clone by15c03 5', mRNA sequence.

ACCESSION BF726995

VERSION BF726995.1 GI:12042906

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 600)

AUTHORS Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.

TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics

JOURNAL Invest. Ophthalmol. Vis. Sci. 41, (2000) In press

COMMENT Contact: Wistow G

Section on Molecular Structure and Function

533 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 571

```
National Eye Institute
          6/331, NIH, Bethesda, MD 20892-2740, USA
          Tel: 301 402 3452
          Fax: 301 496 0078
          Email: graeme@helix.nih.gov
          Plate: 15 row: c column: 03
          Seq primer: M13RP1 reverse primer (ABI).
FEATURES
                 Location/Qualifiers
    source
                 1. .600
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="by15c03"
                 /tissue type="Lens"
                 /dev stage="Adult"
                 /lab host="EMDH10B"
                 /clone lib="Human Lens cDNA (Un-normalized, unamplified):
                 /note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
                 from different adults (both approximately 40 years old)
                 together yielded 20ug of total RNA and 150ng mRNA for cDNA
                 library synthesis. A directionally cloned cDNA library in
                 the pCMVSPORT6 vector was constructed at Life Technologies
                 , essentially following the protocols of the SuperScript
                 Plasmid System full details of which are contained in the
                 manufacturer's Instruction manual
                 (http://www.lifetech.com/). First strand synthesis was
                 carried out using a Not I primer-adapter
                 [5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)15-3']. Not I/blunt
                 end inserts were cloned into the Not I/EcoR V sites in the
                 vector. EST analysis was performed on the unamplified
                 library at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT
              91 a
                    170 c
                            216 q
                                   122 t
                                            1 others
ORIGIN
 Query Match
                     85.0%; Score 308.6; DB 10; Length 600;
 Best Local Similarity
                     94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative
                           0; Mismatches
                                        19; Indels
                                                     0; Gaps
                                                               0;
Qу
         Db
         85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
           Db
        452 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 393
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
        392 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 333
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCCG 264
0y
           Db
        332 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCGTGCCG 273
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
```

```
Db
          272 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 213
QУ
          325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
              Db
         212 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 174
RESULT 12
BM674987/c
LOCUS
           BM674987
                                    616 bp
                                              mRNA
                                                      linear
                                                               EST 27-FEB-2002
DEFINITION UI-E-EJ0-ahn-k-10-0-UI.sl UI-E-EJ0 Homo sapiens cDNA clone
           UI-E-EJ0-ahn-k-10-0-UI 3', mRNA sequence.
ACCESSION
           BM674987
VERSION
           BM674987.1 GI:18984885
KEYWORDS
           EST.
SOURCE
           Homo sapiens (human)
 ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
           1 (bases 1 to 616)
           Bonaldo, M.F., Lennon, G. and Soares, M.B.
 AUTHORS
 TITLE
           Normalization and subtraction: two approaches to facilitate gene
           discovery
 JOURNAL
           Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
           97044477
  PUBMED
           8889548
COMMENT
           Contact: Soares, MB
           Coordinated Laboratory for Computational Genomics
           University of Iowa
           375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
           Tel: 319 335 8250
           Fax: 319 335 9565
           Email: bento-soares@uiowa.edu
           Tissue Procurement: Dr. Gregg Hageman
            CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
            Clone Distribution: Researchers may obtain clones from Research
           Genetics (www.resgen.com).
            The following repetitive elements were found in this cDNA
           sequence: 97-152, >GC rich#Low complexity
           Seq primer: M13 Forward
           POLYA=Yes.
FEATURES
                    Location/Qualifiers
    source
                    1. .616
                    /organism="Homo sapiens"
                    /mol type="mRNA"
                    /db xref="taxon:9606"
                    /clone="UI-E-EJ0-ahn-k-10-0-UI"
                    /tissue_type="fetal eyes, lens, eye anterior segment,
                    optic nerve, retina, Retina Foveal and Macular, RPE and
                    Choroid"
                    /dev_stage="fetal and adult"
                    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                    /clone lib="UI-E-EJ0"
                    /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
```

modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG LIB=UI-E-EJ0

TAG_LIB=UI-E-EJ0
TAG_TISSUE=RPE and Choroid
TAG_SEO=ACCTA"

BASE COUNT 92 a 175 c 225 g 124 t ORIGIN

Query Match 85.0%; Score 308.6; DB 12; Length 616; Best Local Similarity 94.4%; Pred. No. 4.4e-66; Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qу
        Db
      85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
Qу
        434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
Dh
      145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
QУ
        374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
Db
Qу
      205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCG 264
        314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCG 255
Db
     265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qy
        Db
     254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
Qу
      325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
        Db
      194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
```

```
RESULT 13
CA426732/c
```

LOCUS CA426732 625 bp mRNA linear EST 07-NOV-2002 DEFINITION UI-H-FE1-bei-e-23-0-UI.sl NCI_CGAP_FE1 Homo sapiens cDNA clone UI-H-FE1-bei-e-23-0-UI 3', mRNA sequence.

ACCESSION CA426732

VERSION CA426732.1 GI:24789458

```
KEYWORDS
            EST.
SOURCE
            Homo sapiens (human)
  ORGANISM
           Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 625)
  AUTHORS
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL
            Unpublished
COMMENT
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 97-152, >GC rich#Low complexity
            Seg primer: M13 FORWARD
            POLYA=Yes.
FEATURES
                     Location/Qualifiers
     source
                     1. .625
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="UI-H-FE1-bei-e-23-0-UI"
                     /tissue_type="Cell lines"
                     /dev stage="Adult"
                     /lab host="DH10B (Life Technologies)"
                     /clone lib="NCI CGAP FE1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia
                     ) with a modified polylinker; Site 1: EcoR I; Site 2: Not
                     I; NCI CGAP FE1 is a normalized cDNA library derived from
                     a pool of mRNA obtained from 3 cell lines from grade II
                     chondrosarcoma tissues. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CGCTACGGAC. The cell
                     lines were provided by Dr James Martin from the University
                     of Iowa.
                     TAG LIB=UI-H-FE1
                     TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
                     TAG SEQ=CGCTACGGAC"
BASE COUNT
                 95 a
                         175 c
                                  229 q
                                           126 t
ORIGIN
 Query Match
                          85.0%; Score 308.6; DB 14; Length 625;
 Best Local Similarity
                          94.4%; Pred. No. 4.4e-66;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                                 0; Gaps
                                                                             0;
```

```
Qу
         Db
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
QУ
           434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
Db
        145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
        374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
Qу
        205 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCGTCCG 264
           Db
        314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGCGCCCTGCTGCCGC 255
        265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
QУ
           Db
        254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
        325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
Qу
           Dh
        194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
RESULT 14
CA423539/c
LOCUS
         CA423539
                              649 bp
                                      mRNA
                                                   EST 07-NOV-2002
                                            linear
DEFINITION UI-H-FE1-bec-p-13-0-UI.s1 NCI CGAP FE1 Homo sapiens cDNA clone
         UI-H-FE1-bec-p-13-0-UI 3', mRNA sequence.
ACCESSION
         CA423539
VERSION
         CA423539.1 GI:24786265
KEYWORDS
         EST.
SOURCE
         Homo sapiens (human)
 ORGANISM
         Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
            (bases 1 to 649)
 AUTHORS
         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE
         Tumor Gene Index
 JOURNAL
         Unpublished
COMMENT
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: James Martin
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Clone distribution information can be obtained
         from Dr. M. Bento Soares, bento-soares@uiowa.edu
          The following repetitive elements were found in this cDNA
         sequence: 97-152, >GC rich#Low complexity
         Seg primer: M13 FORWARD
         POLYA=Yes.
FEATURES
                Location/Oualifiers
    source
                1. .649
```

```
/mol type="mRNA"
                /db xref="taxon:9606"
                /clone="UI-H-FE1-bec-p-13-0-UI"
                /tissue type="Cell lines"
                /dev stage="Adult"
                /lab host="DH10B (Life Technologies)"
                /clone lib="NCI CGAP FE1"
                /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia
                ) with a modified polylinker; Site 1: EcoR I; Site 2: Not
                I; NCI CGAP FEl is a normalized cDNA library derived from
                a pool of mRNA obtained from 3 cell lines from grade II
                chondrosarcoma tissues. The library was constructed
                according to Bonaldo, Lennon and Soares, Genome Research,
                6:791-806, 1996. First strand cDNA synthesis was primed
                with an oligo-dT primer containing a Not I site. Double
                stranded cDNA was ligated to an EcoR I adaptor, digested
                with Not I, and cloned directionally into pT7T3-Pac
                vector. The oligonucleotide used to prime the synthesis of
                first-strand cDNA contains a library tag sequence that is
                located between the Not I site and the (dT)18 tail. The
                sequence tag for this library is CGCTACGGAC. The cell
                lines were provided by Dr James Martin from the University
                of Iowa.
                TAG LIB=UI-H-FE1
                TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
                TAG_SEQ=CGCTACGGAC"
BASE COUNT
             99 a
                   179 c
                          234 q
                                 137 t
ORIGIN
                    85.0%; Score 308.6; DB 14; Length 649;
 Ouery Match
 Best Local Similarity
                    94.4%; Pred. No. 4.5e-66;
 Matches 320; Conservative
                        0; Mismatches 19; Indels
                                                   0; Gaps
                                                            0;
        Qу
           Db
       Qу
        85 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 144
           Db
       434 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 375
       145 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 204
Qу
           Db
       374 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 315
       Qу
           Db
       314 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGGCGGCGCCGTGCTGCCGCCG 255
       265 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 324
Qу
           Db
       254 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 195
       325 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 363
QУ
           Dh
       194 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 156
```

/organism="Homo sapiens"

```
RESULT 15
BM681750/c
LOCUS
            BM681750
                                     654 bp
                                               mRNA
                                                       linear
                                                                EST 27-FEB-2002
DEFINITION UI-E-EJ0-aik-b-22-0-UI.sl UI-E-EJ0 Homo sapiens cDNA clone
           UI-E-EJ0-aik-b-22-0-UI 3', mRNA sequence.
ACCESSION
           BM681750
VERSION
           BM681750.1 GI:18991646
KEYWORDS
            EST.
SOURCE
           Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 654)
            Bonaldo, M.F., Lennon, G. and Soares, M.B.
  AUTHORS
  TITLE
            Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL
            Genome Res. 6 (9), 791-806 (1996)
  MEDLINE
            97044477
   PUBMED
            8889548
COMMENT
            Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
             The following repetitive elements were found in this cDNA
            sequence: 97-152, >GC rich#Low complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES
                     Location/Qualifiers
     source
                     1. .654
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ0-aik-b-22-0-UI"
                     /tissue type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev stage="fetal and adult"
                     /lab host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone lib="UI-E-EJ0"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-E-EJ0 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
```

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_LIB=UI-E-EJ0

TAG_TISSUE=human lens
TAG_SEQ=CGATTAGCGA"

BASE COUNT 100 a 182 c 234 g 138 t ORIGIN

			Score 308.6;		Length 6	554;		
	cal Similarity	•		•				
Matches	320; Conserv	ative 0;	; Mismatches	19;	Indels	0; G	aps	0;
Qу	25 GCCCTGGATA	CCAACTACTGO	CTTCAGCTCCACG	GAGAAGA?	ACTGCTGCGT	GCGGCA	GCTC	84
Db	494 GCCCTGGAC	CCAACTATTG(CTTCAGCTCCACG	GAGAAGA <i>I</i>	ACTGCTGCGT	GCGGCA	GCTG	435
Qу	85 TACATTGACT	TCCGGAAGGAC	CCTGGGCTGGAAG	TGGATTC	ATGAACCCAA	GGGCTA	CCAT	144
Db	434 TACATTGACT	TCCGCAAGGAC	CCTCGGCTGGAAG	TGGATCC	ACGAGCCCAA	GGGCTA	CCAT	375
Qy	145 GCCAATTTCT	GCTGGGGCC 	CTGTCCCTACATO	TGGAGCCT		GTACAG	CAAG	204
Db	374 GCCAACTTC	GCCTCGGGCCC	CTGCCCCTACATT	TGGAGCC	rgga cacgca	GTACAG	CAAG	315
Qу	205 GTCCTGGCTC					HIIII		
Db	314 GTCCTGGCCC							
Qy	265 CAGGCGCTGC							
Db -	254 CAGGCGCTGC					.GGTGGA	GCAG	195
Qy	325 CTGTCCAACA							
Db	194 CTGTCCAACA	TGATCGTGCGC	CTCCTGCAAGTGC	AGCTGA :	156			

Search completed: October 28, 2003, 00:08:09 Job time: 905.804 secs